SCORE Search Results Details for Application 10552515 and Search Result 20080624_135827_us-10-552-515-1_copy_157_933.rag.

This page gives you Search Results detail for the Application 10552515 and Search Result 20080624_135827_us-10-552-515-1_copy_157_933.rag.

Go Back to previous page

```
                        GenCore version 6.2.1
                  Copyright (c) 1993 - 2008  Biocceleration Ltd.


OM protein - protein search, using sw model

Run on:          June 24, 2008, 15:17:27 ; Search time 267 Seconds
                                           (without alignments)
                                           1751.538 Million cell updates/sec

Title:           US-10-552-515-1_COPY_157_933
Perfect score:   4123
Sequence:        1 QQDVQDGNTTVHYALLSASW.........SELSSHWTPFTVPKASQLQQ 777

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        3405708 seqs, 601879884 residues

Total number of hits satisfying chosen parameters:      3405708

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        A_Geneseq_200711:*
                 1:  geneseqp1980s:*
                 2:  geneseqp1990s:*
                 3:  geneseqp2000:*
                 4:  geneseqp2001:*
                 5:  geneseqp2002:*
                 6:  geneseqp2003a:*
                 7:  geneseqp2003b:*
```

8: geneseqp2004a:*
9: geneseqp2004b:*
10: geneseqp2005:*
11: geneseqp2006:*
12: geneseqp2007:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4123	100.0	933	8	ADT77664	Adt77664 Splice va
2	4123	100.0	933	11	AEL84788	Ael84788 Tumor mar
3	3739	90.7	885	10	AEB13426	Aeb13426 Human pro
4	3572	86.6	843	10	AEB13424	Aeb13424 Human pro
5	3031.5	73.5	898	4	ABG15488	Abg15488 Novel hum
6	1502.5	36.4	920	6	ADB64420	Adb64420 Human pro
7	1482.5	36.0	920	6	ABP58666	Abp58666 Human dih
8	1467.5	35.6	981	8	ADK52114	Adk52114 Human ato
9	1467.5	35.6	981	12	AEN06206	Aen06206 Human eso
10	1461.5	35.4	840	11	AEG11146	Aeg11146 Human tra
11	1456.5	35.3	960	11	AEG11142	Aeg11142 Human tra
12	1452.5	35.2	1017	12	AFB77190	Afb77190 Mouse TM-
13	1437	34.9	1003	7	ADG48280	Adg48280 Human ret
14	1412.5	34.3	913	11	AEH82071	Aeh82071 Human gna
15	1378.5	33.4	1219	4	ABB62812	Abb62812 Drosophil
16	1378.5	33.4	1219	10	AFB95185	Afb95185 Fruit fly
17	1369	33.2	910	6	ADC42854	Adc42854 REMAP pro
18	1369	33.2	910	11	AEL84658	Ael84658 Tumor mar
19	1367.5	33.2	712	11	AEG11145	Aeg11145 Human tra
20	1344	32.6	1075	4	ABB65993	Abb65993 Drosophil
21	1344	32.6	1075	10	AFC04729	Afc04729 Fruit fly
22	1159.5	28.1	1058	4	ABB65022	Abb65022 Drosophil
23	1159.5	28.1	1058	10	AFC01816	Afc01816 Fruit fly
24	1154	28.0	596	6	ADB64387	Adb64387 Human pro
25	1061.5	25.7	594	4	AAB92637	Aab92637 Human pro
26	1061.5	25.7	594	5	ABP43811	Abp43811 FLJ10261
27	1061.5	25.7	594	8	ADJ75429	Adj75429 Marker ge
28	1061.5	25.7	594	8	ADN04848	Adn04848 Antipsori
29	1061.5	25.7	594	11	AEG11143	Aeg11143 Human FLJ
30	1024.5	24.8	782	6	ADX42387	Adx42387 Human col
31	1024.5	24.8	782	7	ADT95905	Adt95905 Colon can
32	1024.5	24.8	782	8	ADQ96288	Adq96288 T cell ac
33	1024.5	24.8	782	8	ADQ96104	Adq96104 T cell ac
34	912.5	22.1	475	6	ADB64962	Adb64962 Human pro

35	873.5	21.2	642	7	ADM05798	Adm05798 Human pro
36	873.5	21.2	642	10	AEC88728	Aec88728 Human cDN
37	873.5	21.2	642	11	AEG11144	Aeg11144 Human FLJ
38	819.5	19.9	443	5	ABP41785	Abp41785 Human ova
39	784.5	19.0	390	5	ABB90382	Abb90382 Human pol
40	735	17.8	139	5	AAE24066	Aae24066 Human pro
41	722.5	17.5	360	4	AAM40391	Aam40391 Human pol
42	711.5	17.3	346	8	ADP29628	Adp29628 Human sec
43	695.5	16.9	608	8	ADQ96298	Adq96298 T cell ac
44	695.5	16.9	608	8	ADQ96286	Adq96286 T cell ac
45	684.5	16.6	483	7	ADM05305	Adm05305 Human pro

ALIGNMENTS

```
RESULT 1
ADT77664
ID   ADT77664 standard; protein; 933 AA.
XX
AC   ADT77664;
XX
DT   15-JUN-2007  (revised)
DT   13-JAN-2005  (first entry)
XX
DE   Splice variant-novel gene expressed in prostate (SV-NGEP) polypeptide.
XX
KW   Splice variant-novel gene expressed in prostate; SV-NGEP; human;
KW   prostate cancer; cytostatic; gene therapy; immunotherapy; BOND_PC;
KW   NGEP long variant; NGEP long variant [Homo sapiens]; GO5886.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          1. .345
FT                   /label= Cytoplasmic
FT   Region          157. .933
FT                   /note= "An immunogenic fragment comprising 8 consecutive
FT                   amino acids that specifically binds to an antibody that
FT                   specifixally binds to a polypeptide comprising amino
FT                   acids 157-933 is referred to in Claim 1"
FT   Region          170. .178
FT                   /note= "Epitope, predicted to bind HLA2-01"
FT   Region          215. .223
FT                   /note= "Epitope, predicted to bind HLA2-01"
FT   Region          258. .266
FT                   /note= "Epitope, predicted to bind HLA2-01"
FT   Domain          346. .368
FT                   /label= Transmembrane
```

```
FT   Domain          369. .421
FT                   /label= External
FT                   /note= "Cell surface"
FT   Region          403. .411
FT                   /note= "Epitope, predicted to bind HLA2-01"
FT   Domain          422. .441
FT                   /label= Transmembrane
FT   Region          427. .435
FT                   /note= "Epitope, predicted to bind HLA2-01"
FT   Domain          442. .501
FT                   /label= Cytoplasmic
FT   Domain          502. .524
FT                   /label= Transmembrane
FT   Domain          525. .543
FT                   /label= External
FT                   /note= "Cell surface"
FT   Domain          544. .566
FT                   /label= Transmembrane
FT   Region          557. .565
FT                   /note= "Epitope, predicted to bind HLA2-01"
FT   Region          562. .570
FT                   /note= "Epitope, predicted to bind HLA2-01"
FT   Domain          567. .586
FT                   /label= Cytoplasmic
FT   Domain          587. .609
FT                   /label= Transmembrane
FT   Domain          610. .714
FT                   /label= External
FT                   /note= "Cell surface"
FT   Domain          715. .737
FT                   /label= Transmembrane
FT   Domain          738. .761
FT                   /label= Cytoplasmic
FT   Domain          762. .784
FT                   /label= Transmembrane
FT   Domain          785. .933
FT                   /label= External
FT                   /note= "Cell surface"
FT   Region          846. .854
FT                   /note= "Epitope, predicted to bind HLA2-01"
XX
PN   WO2004092213-A1.
XX
PD   28-OCT-2004.
XX
PF   05-APR-2004; 2004WO-US010588.
XX
PR   08-APR-2003; 2003US-0461399P.
XX
```

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Pastan I, Bera TK, Lee B;
XX
DR WPI; 2004-758338/74.
DR N-PSDB; ADT77665.
DR PC:NCBI; gi48093524.
XX
PT New Splice Variant-Novel Gene Expressed in Prostate polypeptide or
PT encoding nucleic acid molecule for diagnosing, preventing or treating
PT cancer, especially prostate cancer.
XX
PS Claim 1; SEQ ID NO 1; 88pp; English.
XX
CC The present sequence is the protein sequence of splice variant-novel gene
CC expressed in prostate (SV-NGEP). SV-NGEP is identical to NGEP from amino
CC acid 1-157, diverging from amino acid 158. Expression analysis in 76
CC normal and foetal tissues showed SV-NGEP to be strongly expressed only in
CC a prostate sample. Claimed methods for detecting prostate cancer in a
CC subject comprise: contacting the sample with an antibody that
CC specifically binds a SV-NGEP polypeptide and detecting the formation of
CC an immune complex; or detecting an increase in expression of SV-NGEP
CC polypeptide or mRNA. Antibodies to an SV-NGEP polypeptide can be used to
CC detect metastatic prostate cancer cells at locations other than the
CC prostate. A claimed method for producing an immune response against a
CC cell expressing SV-NGEP, for example in a subject with prostate cancer,
CC comprises administering the polypeptide, or a polynucleotide encoding it,
CC to produce an immune response that decreases growth of the prostate
CC cancer. A claimed method for inhibiting the growth of a malignant cell
CC that expresses SV-NGEP comprises culturing cytotoxic T lymphocytes (CTLs)
CC with SV-NGEP to produce activated CTLs that recognise an NGEP expressing
CC cell, and contacting the malignant cell with the activated CTLs.
CC Alternatively, growth of a malignant cell is inhibited by contact with an
CC antibody that specifically binds an SV-NGEP polypeptide, where the
CC antibody is linked to an effector molecule (chemotherapeutic agent or
CC toxin) that inhibits growth of the malignant cell. This may be performed
CC in vivo. Kits for detecting an SV-NGEP polypeptide or polynucleotide in a
CC sample are also claimed.
CC
CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 933 AA;

Query Match 100.0%; Score 4123; DB 8; Length 933;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 777; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQDVQDGNTTVHYALLSASWAVLCYYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVL 60


Db 157 QQDVQDGNTTVHYALLSASWAVLCYYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVL 216
Qy 61 LEVVPDVPPEYYSCRFRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLL 120
Db 217 LEVVPDVPPEYYSCRFRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLL 276
Qy 121 GIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLNQRQVLFQHWARWGKWNKYQPLDHVR 180
Db 277 GIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLNQRQVLFQHWARWGKWNKYQPLDHVR 336
Qy 181 RYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPL 240
Db 337 RYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPL 396
Qy 241 CLDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSD 300
Db 397 CLDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSD 456
Qy 301 YEDTEERPRPQFAASAPMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLV 360
Db 457 YEDTEERPRPQFAASAPMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLV 516
Qy 361 SIILYRAIMAIVVSRSGNTLLAAWASRIASLTGSVVNLVFILILSKIYVSLAHVLTRWEM 420
Db 517 SIILYRAIMAIVVSRSGNTLLAAWASRIASLTGSVVNLVFILILSKIYVSLAHVLTRWEM 576
Qy 421 HRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPGNYHTLFGVRNEECAAGGC 480
Db 577 HRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPGNYHTLFGVRNEECAAGGC 636
Qy 481 LIELAQELLVIMVGKQVINNMQEVLIPKLKGWWQKFRLRSKKRKAGASAGASQGPWEDDY 540
Db 637 LIELAQELLVIMVGKQVINNMQEVLIPKLKGWWQKFRLRSKKRKAGASAGASQGPWEDDY 696
Qy 541 ELVPCEGLFDEYLEMVLQFGFVTIFVAACPLAPLFALLNNWVEIRLDARKFVCEYRRPVA 600
Db 697 ELVPCEGLFDEYLEMVLQFGFVTIFVAACPLAPLFALLNNWVEIRLDARKFVCEYRRPVA 756
Qy 601 ERAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPRAYYRWTRAHDLRGFLNFTLARAP 660
Db 757 ERAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPRAYYRWTRAHDLRGFLNFTLARAP 816
Qy 661 SSFAAAHNRTCRYRAFRDDDGHYSQTYWNLLAIRLAFVIVFEHVVFSVGRLLDLLVPDIP 720
Db 817 SSFAAAHNRTCRYRAFRDDDGHYSQTYWNLLAIRLAFVIVFEHVVFSVGRLLDLLVPDIP 876
Qy 721 ESVEIKVKREYYLAKQALAENEVLFGTNGTKDEQPKGSELSSHWTPFTVPKASQLQQ 777

```
Db        877 ESVEIKVKREYYLAKQALAENEVLFGTNGTKDEQPKGSELSSHWTPFTVPKASQLQQ 933


RESULT 2
AEL84788
ID   AEL84788 standard; protein; 933 AA.
XX
AC   AEL84788;
XX
DT   18-OCT-2007  (revised)
DT   15-JUN-2007  (revised)
DT   28-DEC-2006  (first entry)
XX
DE   Tumor marker gene NGEP SEQ ID NO 155.
XX
KW   cytostatic; diagnosis; prognosis; tumor marker; gene expression;
KW   drug screening; cancer; neoplasm; NGEP; BOND_PC; NGEP long variant;
KW   GO5886.
XX
OS   Homo sapiens.
XX
PN   WO2006110593-A2.
XX
PD   19-OCT-2006.
XX
PF   07-APR-2006; 2006WO-US013172.
XX
PR   07-APR-2005; 2005US-0669342P.
PR   11-OCT-2005; 2005US-0725982P.
XX
PA   (MACR-) MACROGENICS INC.
XX
PI   Von Haller PD,  Schummer M,  Meyer DW,  Schubert LA,  Tjoelker LW;
XX
DR   WPI; 2006-814687/82.
DR   N-PSDB; AEL84787.
DR   REFSEQ; NP_001001891.
DR   PC:NCBI; gi48093524.
XX
PT   Detecting or diagnosing cancer in a subject comprises determining
PT   expression of at least one gene, and comparing level of expression to a
PT   control sample from a normal subject, where increased expression level
PT   indicates cancer.
XX
PS   Claim 8; SEQ ID NO 155; 583pp; English.
XX
CC   The invention describes a method of detecting or diagnosing cancer in a
CC   subject comprising determining the expression level of at least one gene,
CC   and comparing the level of expression to a corresponding control sample
```

CC from a normal subject, where cancer is detected or diagnosed if there is
CC an increase in the expression level of the gene relative to the
CC expression in the control sample. Also described are: identifying a
CC compound to be tested for its ability to prevent, treat, manage, or
CC ameliorate cancer or its symptom; a compound identified by the method;
CC treating cancer in a patient; treating a cancer in a subject that is
CC fully or partially refractory to a first treatment in a patient; and a
CC pharmaceutical composition comprising an amount of an antibody selected
CC from anti-SLC12A2, anti-FLJ23375, anti-GRM5, anti-TAS2R1, anti-NRXN2,
CC anti-C14orf160, anti-MGC 15668, anti-MGC33486, anti-TMEM16F, anti-FAT,
CC anti-KIAA0195, anti-LRFN, anti-NFASC, anti-BAT2D1, anti-MGC2963, anti-
CC KIAA0685, anti-EDG3, anti-GGTL3, anti-PLVAP, anti-FLJ31528, anti-
CC FLJ90709, anti-VEZATIN, anti-TMPRSS9, anti-ATP13A5, anti-PKHD1L1, anti-
CC C2orf18, anti-ANKRD22, anti-FAM62B, anti-LOC57168, anti-CDKAL1, anti-
CC SLC39A3v1, anti-SLC39A3v2, anti-BAT5, anti-TM9SF4, anti-DC2, anti-VAPB,
CC anti-XTP3TPB, anti-TACSTD2, anti-FNDC3A, anti-GK001, anti-OCIAD2, anti-
CC PR01855, anti-C20orf3, anti-SDFR1, anti-FLJ20481, anti-LENG4, anti-
CC FLJ12443, anti-ARP5 Long, anti-ARP5 Short, anti-TMD0645, anti-NGEP, anti-
CC IL1RAP1, anti-PLXNB1, anti-ATP2B2, anti-FLJ11848, anti-ENTPD2, anti-
CC PPM1H, anti-KRTKAP3, anti-KCNC3, anti-TM9SF1, anti-ULBP1, anti-C19orf26,
CC anti-KIAA830, anti-KIAA1244, anti-KIAA1797, anti-MGC26856, anti-NETO2,
CC anti-SUSD2, anti-FOLR2, anti-EMR2, ENTPD1, anti-ATP10B, anti-PTK7, anti-
CC FLJ14681, anti-C20orf22, anti-FLJ14281, anti-FAM8A1, anti-TMED7, anti-
CC C20orf108, anti-ATAD1, anti-GPR154, anti-C14orf27, anti-OSAP, anti-
CC FAD104, anti-FLJ90492, anti-SLC27A3, anti-RON, anti-ATP13A1, anti-
CC DKFZP564D166, anti-ESSPL, anti-EXTL3, anti-KAI1, anti-KIAA0960, anti-
CC MTRNL, anti-SLC27A1, anti-GRIA, anti-OR4M1, anti-KIAA1679, or anti-UPK-1b
CC antibody, and a pharmaceutical carrier. The methods are useful for
CC detecting, diagnosing, and treating cancer, e.g. colon, lung, ovary,
CC prostate, pancreas, or bladder cancer. This is the amino acid sequence of
CC NGEP, altered levels of expression are useful in the diagnosis or
CC prognosis of cancer.
CC
CC Revised record issued on 18-OCT-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 933 AA;

Query Match 100.0%; Score 4123; DB 11; Length 933;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 777; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 QQDVQDGNTTVHYALLSASWAVLCYYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        157 QQDVQDGNTTVHYALLSASWAVLCYYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVL 216

Qy         61 LEVVPDVPPEYYSCRFRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        217 LEVVPDVPPEYYSCRFRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLL 276
```

```
Qy          121 GIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLNQRQVLFQHWARWGKWNKYQPLDHVR 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          277 GIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLNQRQVLFQHWARWGKWNKYQPLDHVR 336

Qy          181 RYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPL 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          337 RYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPL 396

Qy          241 CLDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSD 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          397 CLDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSD 456

Qy          301 YEDTEERPRPQFAASAPMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLV 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          457 YEDTEERPRPQFAASAPMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLV 516

Qy          361 SIILYRAIMAIVVSRSGNTLLAAWASRIASLTGSVVNLVFILILSKIYVSLAHVLTRWEM 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          517 SIILYRAIMAIVVSRSGNTLLAAWASRIASLTGSVVNLVFILILSKIYVSLAHVLTRWEM 576

Qy          421 HRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPGNYHTLFGVRNEECAAGGC 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          577 HRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPGNYHTLFGVRNEECAAGGC 636

Qy          481 LIELAQELLVIMVGKQVINNMQEVLIPKLKGWWQKFRLRSKKRKAGASAGASQGPWEDDY 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          637 LIELAQELLVIMVGKQVINNMQEVLIPKLKGWWQKFRLRSKKRKAGASAGASQGPWEDDY 696

Qy          541 ELVPCEGLFDEYLEMVLQFGFVTIFVAACPLAPLFALLNNWVEIRLDARKFVCEYRRPVA 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          697 ELVPCEGLFDEYLEMVLQFGFVTIFVAACPLAPLFALLNNWVEIRLDARKFVCEYRRPVA 756

Qy          601 ERAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPRAYYRWTRAHDLRGFLNFTLARAP 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          757 ERAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPRAYYRWTRAHDLRGFLNFTLARAP 816

Qy          661 SSFAAAHNRTCRYRAFRDDDGHYSQTYWNLLAIRLAFVIVFEHVVFSVGRLLDLLVPDIP 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          817 SSFAAAHNRTCRYRAFRDDDGHYSQTYWNLLAIRLAFVIVFEHVVFSVGRLLDLLVPDIP 876

Qy          721 ESVEIKVKREYYLAKQALAENEVLFGTNGTKDEQPKGSELSSHWTPFTVPKASQLQQ 777
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          877 ESVEIKVKREYYLAKQALAENEVLFGTNGTKDEQPKGSELSSHWTPFTVPKASQLQQ 933


RESULT 3
AEB13426
ID   AEB13426 standard; protein; 885 AA.
```

XX
AC AEB13426;
XX
DT 22-SEP-2005 (first entry)
XX
DE Human prostate specific polypeptide #2.
XX
KW Screening; diagnosis; drug delivery; prostate specific polypeptide;
KW cancer; prostate tumor; cytostatic; neoplasm.
XX
OS Homo sapiens.
XX
PN WO2005062788-A2.
XX
PD 14-JUL-2005.
XX
PF 16-DEC-2004; 2004WO-US042406.
XX
PR 22-DEC-2003; 2003US-0531809P.
XX
PA (AVAL-) AVALON PHARM INC.
XX
PI Weigle B, Ebner R;
XX
DR WPI; 2005-497793/50.
DR N-PSDB; AEB13425.
XX
PT Novel isolated prostate specific polypeptide, useful for treating cancer,
PT and identifying agent that modulates activity of cancer related gene.
XX
PS Claim 12; SEQ ID NO 5; 59pp; English.
XX
CC The invention relates to an isolated prostate specific polypeptide
CC comprising one or more immunogenic fragments. The invention also relates
CC to a method of identifying an agent that modulates the activity of a
CC cancer related gene involving contacting a compound with a cell
CC containing a gene under conditions promoting the expression of the gene,
CC detecting a difference in expression of the gene relative to when the
CC compound is not present and identifying an agent that modulates the
CC activity of a cancer related gene, a method of identifying an anti-
CC neoplastic agent involving contacting a cell exhibiting neoplastic
CC activity with a compound first identified as a cancer related gene
CC modulator using and determining a decrease in neoplastic activity after
CC contacting, when compared to when the contacting does not occur, or
CC administering an agent first identified to an animal exhibiting a cancer
CC condition and detecting a decrease in cancerous condition, a method of
CC determining the cancerous status of a cell involving determining an
CC increase in the level of expression in a cell of a gene where an elevated
CC expression relative to a known non-cancerous cell indicates a cancerous

CC state or potentially cancerous state, an antibody that reacts with a
CC prostate specific polypeptide, an immunoconjugate comprising the antibody
CC and a cytotoxic agent, a method of treating cancer involving contacting a
CC cancerous cell in vivo with an agent having activity against a prostate
CC specific polypeptide and an immunogenic composition the prostate specific
CC polypeptide. The prostate specific polypeptide is useful for identifying
CC an agent that modulates the activity of a cancer related gene. The
CC immunogenic composition is useful for treating cancer, preferably
CC prostate cancer in an animal, e.g. human, which involves administering
CC the immunogenic composition that is sufficient to elicit the production
CC of cytotoxic T lymphocytes specific for the prostate specific
CC polypeptide. The invention is useful for identifying anti-neoplastic
CC agents. This sequence represents a human prostate specific polypeptide of
CC the invention.
XX
SQ Sequence 885 AA;

Query Match 90.7%; Score 3739; DB 10; Length 885;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 QQDVQDGNTTVHYALLSASWAVLCYYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        158 QQDVQDGNTTVHYALLSASWAVLCYYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVL 217

Qy         61 LEVVPDVPPEYYSCRFRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 LEVVPDVPPEYYSCRFRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLL 277

Qy        121 GIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLNQRQVLFQHWARWGKWNKYQPLDHVR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 GIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLNQRQVLFQHWARWGKWNKYQPLDHVR 337

Qy        181 RYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        338 RYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPL 397

Qy        241 CLDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSD 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        398 CLDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSD 457

Qy        301 YEDTEERPRPQFAASAPMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLV 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        458 YEDTEERPRPQFAASAPMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLV 517

Qy        361 SIILYRAIMAIVVSRSGNTLLAAWASRIASLTGSVVNLVFILILSKIYVSLAHVLTRWEM 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        518 SIILYRAIMAIVVSRSGNTLLAAWASRIASLTGSVVNLVFILILSKIYVSLAHVLTRWEM 577
```

```
Qy        421 HRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPGNYHTLFGVRNEECAAGGC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        578 HRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPGNYHTLFGVRNEECAAGGC 637

Qy        481 LIELAQELLVIMVGKQVINNMQEVLIPKLKGWWQKFRLRSKKRKAGASAGASQGPWEDDY 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        638 LIELAQELLVIMVGKQVINNMQEVLIPKLKGWWQKFRLRSKKRKAGASAGASQGPWEDDY 697

Qy        541 ELVPCEGLFDEYLEMVLQFGFVTIFVAACPLAPLFALLNNWVEIRLDARKFVCEYRRPVA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        698 ELVPCEGLFDEYLEMVLQFGFVTIFVAACPLAPLFALLNNWVEIRLDARKFVCEYRRPVA 757

Qy        601 ERAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPRAYYRWTRAHDLRGFLNFTLARAP 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        758 ERAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPRAYYRWTRAHDLRGFLNFTLARAP 817

Qy        661 SSFAAAHNRTCRYRAFRDDDGHYSQTYWNLLAIRLAFVIVFE 702
              |||||||||||||||||||||||||||||||||||||||||||
Db        818 SSFAAAHNRTCRYRAFRDDDGHYSQTYWNLLAIRLAFVIVFE 859


RESULT 4
AEB13424
ID   AEB13424 standard; protein; 843 AA.
XX
AC   AEB13424;
XX
DT   22-SEP-2005  (first entry)
XX
DE   Human prostate specific polypeptide #1.
XX
KW   Screening; diagnosis; drug delivery; prostate specific polypeptide;
KW   cancer; prostate tumor; cytostatic; neoplasm.
XX
OS   Homo sapiens.
XX
PN   WO2005062788-A2.
XX
PD   14-JUL-2005.
XX
PF   16-DEC-2004; 2004WO-US042406.
XX
PR   22-DEC-2003; 2003US-0531809P.
XX
PA   (AVAL-) AVALON PHARM INC.
XX
PI   Weigle B,  Ebner R;
XX
DR   WPI; 2005-497793/50.
```

DR N-PSDB; AEB13423.
XX
PT Novel isolated prostate specific polypeptide, useful for treating cancer,
PT and identifying agent that modulates activity of cancer related gene.
XX
PS Claim 12; SEQ ID NO 3; 59pp; English.
XX
CC The invention relates to an isolated prostate specific polypeptide
CC comprising one or more immunogenic fragments. The invention also relates
CC to a method of identifying an agent that modulates the activity of a
CC cancer related gene involving contacting a compound with a cell
CC containing a gene under conditions promoting the expression of the gene,
CC detecting a difference in expression of the gene relative to when the
CC compound is not present and identifying an agent that modulates the
CC activity of a cancer related gene, a method of identifying an anti-
CC neoplastic agent involving contacting a cell exhibiting neoplastic
CC activity with a compound first identified as a cancer related gene
CC modulator using and determining a decrease in neoplastic activity after
CC contacting, when compared to when the contacting does not occur, or
CC administering an agent first identified to an animal exhibiting a cancer
CC condition and detecting a decrease in cancerous condition, a method of
CC determining the cancerous status of a cell involving determining an
CC increase in the level of expression in a cell of a gene where an elevated
CC expression relative to a known non-cancerous cell indicates a cancerous
CC state or potentially cancerous state, an antibody that reacts with a
CC prostate specific polypeptide, an immunoconjugate comprising the antibody
CC and a cytotoxic agent, a method of treating cancer involving contacting a
CC cancerous cell in vivo with an agent having activity against a prostate
CC specific polypeptide and an immunogenic composition the prostate specific
CC polypeptide. The prostate specific polypeptide is useful for identifying
CC an agent that modulates the activity of a cancer related gene. The
CC immunogenic composition is useful for treating cancer, preferably
CC prostate cancer in an animal, e.g. human, which involves administering
CC the immunogenic composition that is sufficient to elicit the production
CC of cytotoxic T lymphocytes specific for the prostate specific
CC polypeptide. The invention is useful for identifying anti-neoplastic
CC agents. This sequence represents a human prostate specific polypeptide of
CC the invention.
XX
SQ Sequence 843 AA;

Query Match 86.6%; Score 3572; DB 10; Length 843;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 671; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQDVQDGNTTVHYALLSASWAVLCYYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVL 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 158 QQDVQDGNTTVHYALLSASWAVLCYYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVL 217

```
Qy          61 LEVVPDVPPEYYSCRFRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLL 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         218 LEVVPDVPPEYYSCRFRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLL 277

Qy         121 GIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLNQRQVLFQHWARWGKWNKYQPLDHVR 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         278 GIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLNQRQVLFQHWARWGKWNKYQPLDHVR 337

Qy         181 RYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPL 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         338 RYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPL 397

Qy         241 CLDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSD 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         398 CLDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSD 457

Qy         301 YEDTEERPRPQFAASAPMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLV 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         458 YEDTEERPRPQFAASAPMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLV 517

Qy         361 SIILYRAIMAIVVSRSGNTLLAAWASRIASLTGSVVNLVFILILSKIYVSLAHVLTRWEM 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         518 SIILYRAIMAIVVSRSGNTLLAAWASRIASLTGSVVNLVFILILSKIYVSLAHVLTRWEM 577

Qy         421 HRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPGNYHTLFGVRNEECAAGGC 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         578 HRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPGNYHTLFGVRNEECAAGGC 637

Qy         481 LIELAQELLVIMVGKQVINNMQEVLIPKLKGWWQKFRLRSKKRKAGASAGASQGPWEDDY 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         638 LIELAQELLVIMVGKQVINNMQEVLIPKLKGWWQKFRLRSKKRKAGASAGASQGPWEDDY 697

Qy         541 ELVPCEGLFDEYLEMVLQFGFVTIFVAACPLAPLFALLNNWVEIRLDARKFVCEYRRPVA 600
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         698 ELVPCEGLFDEYLEMVLQFGFVTIFVAACPLAPLFALLNNWVEIRLDARKFVCEYRRPVA 757

Qy         601 ERAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPRAYYRWTRAHDLRGFLNFTLARAP 660
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         758 ERAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPRAYYRWTRAHDLRGFLNFTLARAP 817

Qy         661 SSFAAAHNRTC 671
               ||||||||||
Db         818 SSFAAAHNRTC 828


RESULT 5
ABG15488
ID   ABG15488 standard; protein; 898 AA.
XX
```

AC ABG15488;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #15479.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS79675.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 45847; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity

```
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC   amino acid sequences of the invention. Note: The sequence data for this
CC   patent did not appear in the printed specification, but was obtained in
CC   electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 898 AA;

  Query Match             73.5%;  Score 3031.5;  DB 4;  Length 898;
  Best Local Similarity   91.2%;  Pred. No. 6.3e-316;
  Matches  578;  Conservative    2;  Mismatches   11;  Indels   43;  Gaps    2;

Qy          1 QQDVQDGNTTVHYALLSASWAVLCYYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVL 60
              |||||||||||||||||||||||||||||||||||||: | :          |||||||||
Db        250 QQDVQDGNTTVHYALLSASWAVLCYYAEDLRLKLPLQDYPTRPPTGRPACCAWLGIPNVL 309

Qy         61 LEVVPDVPPEYYSCRFRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 LEVVPDVPPEYYSCRFRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLL 369

Qy        121 GIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLNQRQVLFQHWARWGKWNKYQPLDHVR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 GIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLNQRQVLFQHWARWGKWNKYQPLDHVR 429

Qy        181 RYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 RYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPL 489

Qy        241 CLDCPFWLLSSACALAQ----AGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRW 296
              |||||||||||||||||    ||||||||||||||||||||||||||||||||||||||
Db        490 CLDCPFWLLSSACALAQVREEAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRW 549

Qy        297 DCSDYEDTEERPRPQFAASAPMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMVAVVV 356
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 DCSDYEDTEERPRPQFAASAPMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMVAVVV 609

Qy        357 MCLVSIILYRAIMAIVVSRSGNTLLAAWASRIASLTGSVVNLVFILILSKIYVSLAHVLT 416
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 MCLVSIILYRAIMAIVVSRSGNTLLAAWASRIASLTGSVVNLVFILILSKIYVSLAHVLT 669

Qy        417 RWEMHRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPGNYHTLFGVRNEECA 476
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 RWEMHRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPGNYHTLFGVRNEECA 729

Qy        477 AGGCLIELAQELLVIMVGKQVINNMQEVLIPKLKGWWQKFRLRSKKRKAGASAGASQGPW 536
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 AGGCLIELAQELLVIMVGKQVINNMQEVLIPKLKGWWQKFRLRSKKRKAGASAGASQGPW 789
```

```
Qy        537 EDDYELVPCEGLFDEYLEM----------------------------------------VL 557
              ||||||||||||||||||                                        ||
Db        790 EDDYELVPCEGLFDEYLEMGAGFCPNACPELVPELTEPEKARDQPEARSAGQDSRPEAVL 849

Qy        558 QFGFVTIFVAACPLAPLFALLNNWVEIRLDARKF 591
              ||||||||||||||||||||||||||||||||||
Db        850 QFGFVTIFVAACPLAPLFALLNNWVEIRLDARKF 883


RESULT 6
ADB64420
ID   ADB64420 standard; protein; 920 AA.
XX
AC   ADB64420;
XX
DT   15-JUN-2007  (revised)
DT   04-DEC-2003  (first entry)
XX
DE   Human protein encoded by clone FEBRA20031280.
XX
KW   Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration;
KW   cell regeneration; membrane protein; signal transduction-related protein;
KW   transcription-related protein; osteoporosis; neurological disease;
KW   cancer; tumour; BOND_PC; transmembrane protein 16D;
KW   transmembrane protein 16D (eight membrane-spanning domains);
KW   transmembrane protein 16D [Homo sapiens]; TMEM16D; FLJ34221; FLJ34272;
KW   FLJ35277; MGC130026; unnamed protein product;
KW   unnamed protein product [Homo sapiens].
XX
OS   Homo sapiens.
XX
PN   EP1308459-A2.
XX
PD   07-MAY-2003.
XX
PF   28-MAR-2002; 2002EP-00007401.
XX
PR   05-NOV-2001; 2001JP-00379298.
PR   25-JAN-2002; 2002US-0350978P.
XX
PA   (HELI-) HELIX RES INST.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI   Isogai T,  Sugiyama T,  Otsuki T,  Wakamatsu A,  Sato H,  Ishii S;
PI   Yamamoto J,  Isono Y,  Hio Y,  Otsuka K,  Nagai K,  Irie R,  Tamechika I;
PI   Seki N,  Yoshikawa T,  Otsuka M,  Nagahari K,  Masuho Y;
XX
DR   WPI; 2003-450961/43.
DR   N-PSDB; ADB62450.
```

DR PC:NCBI; gi30520318.
XX
PT New polynucleotides and polypeptides, useful for developing a diagnostic
PT marker or medicines for regulation of their expression and activity, or
PT as targets of gene therapy.
XX
PS Claim 1; Page; 222pp; English.
XX
CC The invention discloses a polynucleotide comprising a sequence selected
CC from 1970 fully defined nucleotide sequences which encode novel
CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide
CC or its partial peptide, an antibody binding to the polypeptide or peptide
CC of the polynucleotide, immunologically assaying the polypeptide or
CC peptide of the polynucleotide by contacting the polypeptide or peptide
CC with the antibody of the encoded protein, and observing the binding
CC between the two, a transformant carrying the polynucleotide in an
CC expressible manner and an antisense polynucleotide. The oligonucleotide
CC is useful as a primer for synthesising the polynucleotide, or as a probe
CC for detecting the polynucleotide. The polynucleotides and encoded
CC proteins are useful as pharmaceutical agents and many disease-related
CC genes may be included in them, for developing a diagnostic marker or
CC medicines for regulation of their expression and activity, or as targets
CC of gene therapy. The genes are involved in tissue and/or cell
CC regeneration. Membrane proteins, signal transduction-related proteins,
CC transcription-related proteins, disease-related proteins and genes
CC encoding them can be used as indicators for diseases (e.g. osteoporosis,
CC neurological diseases, cancer, tumours. The cDNA may be used to regulate
CC the activity or expression of the encoded protein to treat diseases. The
CC sequence presented is a protein of the invention. Note: Some of the
CC sequence data for this patent is not represented in the printed
CC specification, but is based on sequence information supplied by the
CC European Patent Office.
CC
CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 920 AA;

Query Match 36.4%; Score 1502.5; DB 6; Length 920;
Best Local Similarity 40.4%; Pred. No. 2.5e-151;
Matches 328; Conservative 145; Mismatches 270; Indels 69; Gaps 20;

```
Qy          8 NTTVHYALLSASWAVLCYYAEDLRLKLPLQE----LPNQASNWS------AGLLAWLGIP 57
              |: : :  | | | ||  ||| : :::| :     || :    |      : |  ||
Db        122 NSDIIFVKLHAPWEVLGRYAEQMNVRMPFRRKIYYLPRRYKFMSRIDKQISRLRRWLPKK 181

Qy         58 NVLL--EVVPDVPP-EYYSCRFRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTPYGH 114
                : |  | :||:   : |:  |   ::  |:   |::||| :  | :|:  || :  |
Db        182 PMRLDKETLPDLEENDCYTAPFSQQRIHHFI-IHNKETFFNNATRSRIVHHILQRIKY-E 239
```

```
Qy        115 EKKNLLGIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLNQRQVLFQHWARWGKWNKYQ 174
              | || :|:::||  |   ||||||:| :::          | | :|:: || || | |||
Db        240 EGKNKIGLNRLLTNGSYEAAFPLHEGSYRSKNSIRTHGAENHRHLLYECWASWGVWYKYQ 299

Qy        175 PLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDS 234
              ||| ||||||||: |||||||:||| | ||| :|  ||| |   :     ::|:| : |
Db        300 PLDLVRRYFGEKIGLYFAWLGWYTGMLFPAAFIGLFVFLYGVTTLDHSQVSKEVCQATDI 359

Qy        235 FEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLA 293
                ||:|   |||  || :|  |:   |||:| ||||::|||:|| : ||:|||: | :|
Db        360 I-MCPVCDKYCPFMRLSDSCVYAKVTHLFDNGATVFFAVFMAVWATVFLEFWKRRRAVIA 418

Qy        294 YRWDCSDYEDTEERPRPQFAAS-APMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMV 352
              | ||  |:|: ||  |||| |  :     |||:|: |||      :  |::  :  |  |:
Db        419 YDWDLIDWEEEEEEIRPQFEAKYSKKERMNPISGKPEPYQAFTDKCSRLIVSASGIFFMI 478

Qy        353 AVVVMCLVSIILYRAIMAIVVSRSGNTLLA-AWA-----SRIASLTGSVV--NLVFILIL 404
               ||:  :  |:::|| |          :|  |  ||      |::|: ||: |  |   |::|
Db        479 CVVIAAVFGIVIYRVVTV-------STFAAFKWALIRNNSQVAT-TGTAVCINFCIIMLL 530

Qy        405 SKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPGNY 464
              : :|  :| ::||  |  ||::::|::||||:|:|||||  ||  ||||| ||| |:|| |
Db        531 NVLYEKVALLLTNLEQPRTESEWENSFTLKMFLFQFVNLNSSTFYIAFFLGRFTGHPGAY 590

Qy        465 HTLFG-VRNEECAAGGCLIELAQELLVIMVGKQVINNMQEVLIPKLKGWWQKFRLRSKKR 523
                |    | |||   ||||:|  :: :||| ||  ||  |:  | :: || :   |  ::
Db        591 LRLINRWRLEECHPSGCLIDLCMQMGIIMVLKQTWNNFMELGYPLIQNWWTR---RKVRQ 647

Qy        524 KAGASAGASQGPWEDDYELVPCE--GLFDEYLEMVLQFGFVTIFVAACPLAPLFALLNNW 581
              : |     |   || || | |    |||||||||:||||| |||||| ||||| |||||
Db        648 EHGPERKISFPQWEKDYNLQPMNAYGLFDEYLEMILQFGFTTIFVAAFPLAPLLALLNNI 707

Qy        582 VEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPRAYYR 641
              :|||||| ||| ::|||:| ||:|||||: || |:  |:||:||||::| :|||:||  |
Db        708 IEIRLDAYKFVTQWRRPLASRAKDIGIWYGILEGIGILSVITNAFVIAITSDFIPRLVYA 767

Qy        642 W----------TRAHDLRGFLNFTLA--------------RAPSSFAAAHNRTCRYRAFR 677
              :           : |::| :|:                 | |:    : |||| :|
Db        768 YKYGPCAGQGEAGQKCMVGYVNASLSVFRISDFENRSEPESDGSEFSGTPLKYCRYRDYR 827

Qy        678 DDDGH-----YSQTYWNLLAIRLAFVIVFEHVVFSVGRLLDLLVPDIPESVEIKVKREYY 732
              |          |:  :|::|| ||||:|||||:|| :  |:  |:||:|: :  :::|| |
Db        828 DPPHSLVPYGYTLQFWHVLAARLAFIIVFEHLVFCIKHLISYLIPDLPKDLRDRMRREKY 887

Qy        733 LAKQALAENEVLFGTNGTKDEQPKGSELSSHW 764
              | :: : | |:       |: :  |    : |
Db        888 LIQEMMYEAELERLQKERKERKKNGKAHHNEW 919
```

```
RESULT 7
ABP58666
ID   ABP58666 standard; protein; 920 AA.
XX
AC   ABP58666;
XX
DT   24-MAR-2003  (first entry)
XX
DE   Human dihydropyrimidinase related protein 1-101.20.
XX
KW   Human; dihydropyrimidinase related protein 1-101.20;
KW   recombinant production; gene therapy; psychosis; development disorder;
KW   uracil-related metabolic disorder; thymine-related metabolic disorder;
KW   pyrimidine metabolic disorder.
XX
OS   Homo sapiens.
XX
PN   CN1364894-A.
XX
PD   21-AUG-2002.
XX
PF   10-JAN-2001; 2001CN-00105195.
XX
PR   10-JAN-2001; 2001CN-00105195.
XX
PA   (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2003-000532/01.
DR   N-PSDB; ABZ57080.
XX
PT   New polypeptide-human dihydropyrimidinase relative protein 1-101, 20 and
PT   polynucleotide for encoding such polypeptide.
XX
PS   Claim 1; Page 28-30 (Disclosure); 36pp; Chinese.
XX
CC   The invention relates to human dihydropyrimidinase related protein 1-
CC   101.20 (ABP58666) and nucleic acids encoding it (ABZ57080). The protein
CC   has a molecular weight of 101.2 kD. The invention also relates to a
CC   method for the recombinant production of the protein, an antagonist of
CC   the protein, and the use of the protein, gene and antagonist in
CC   therapeutic applications. Dihydropyrimidinase related protein 1-101.20
CC   can be used in the treatment of a variety of diseases such as psychosis,
CC   development disorders and uracil- and thymine-related metabolic
CC   disorders. The present sequence represents human dihydropyrimidinase
CC   related protein 1-101.20
XX
```

SQ Sequence 920 AA;

Query Match 36.0%; Score 1482.5; DB 6; Length 920;
Best Local Similarity 40.0%; Pred. No. 3.6e-149;
Matches 325; Conservative 146; Mismatches 272; Indels 69; Gaps 20;

```
Qy          8 NTTVHYALLSASWAVLCYYAEDLRLKLPLQE----LPNQASNWS------AGLLAWLGIP 57
              |: : :  | | | ||  ||| : :::| :     || :    |       :    ||
Db        122 NSDIIFVKLHAPWEVLGRYAEQMNVRMPFRRKIYYLPRRYKFMSRIDKQISRFRRWLPKK 181

Qy         58 NVLL--EVVPDVPP-EYYSCRFRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTPYGH 114
              : |  | :|||:   : |:  |   ::  |:   |::|||  :  | :|:  || :  |
Db        182 PMRLDKETLPDLEENDCYTAPFSQQRIHHFI-IHNKETFFNNATRSRIVHHILQRIKY-E 239

Qy        115 EKKNLLGIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLNQRQVLFQHWARWGKWNKYQ 174
              | || :|:::||   |   ||||||:| :::          | | :|:: || || | |||
Db        240 EGKNKIGLNRLLTNGSYEAAFPLHEGSYRSKNSIRTHGAENHRHLLYECWASWGVWYKYQ 299

Qy        175 PLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDS 234
              ||| ||||||||: |||||||:||| | ||| :|  ||| |   :     ::|:| : |
Db        300 PLDLVRRYFGEKIGLYFAWLGWYTGMLFPAAFIGLFVFLYGVTTLDHSQVSKEVCQATDI 359

Qy        235 FEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLA 293
                |||:|   |||  || :|  |:   |||:| |||||::|||:|| : ||:|||: | :|
Db        360 I-MCPVCDKYCPFMRLSDSCVYAKVTHLFDNGATVFFAVFMAVWATVFLEFWKRRRAVIA 418

Qy        294 YRWDCSDYEDTEERPRPQFAAS-APMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMV 352
              | ||  |:|: ||  |||| |  :     |||:|: |||     :  |::  :  |  |:
Db        419 YDWDLIDWEEEEEEIRPQFEAKYSKKERMNPISGKPEPYQAFTDKCSRLIVSASGIFFMI 478

Qy        353 AVVVMCLVSIILYRAIMAIVVSRSGNTLLA-AWA-----SRIASLTGSVV--NLVFILIL 404
              ||:  :  |::|| :         :|  |  ||     |::|: ||: |  |   |::|
Db        479 CVVIAAVFGIVIYRVVTV-------STFAAFKWALIRNNSQVAT-TGTAVCINFCIIMLL 530

Qy        405 SKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPGNY 464
              : :|  :| :||  |  ||::::|::||||:|:|||||  ||  ||||| ||| |:|| |
Db        531 NVLYEKVALLLTNLEQPRTESEWENSFTLKMFLFQFVNLNSSTFYIAFFLGRFTGHPGAY 590

Qy        465 HTLFG-VRNEECAAGGCLIELAQELLVIMVGKQVINNMQEVLIPKLKGWWQKFRLRSKKR 523
                |    | |||   ||||:|  :: :||| ||  ||  |:  | :: || :   |  ::
Db        591 LRLINRWRLEECHPSGCLIDLCMQMGIIMVLKQTWNNFMELGYPLIQNWWTR---RKVRQ 647

Qy        524 KAGASAGASQGPWEDDYELVPCE--GLFDEYLEMVLQFGFVTIFVAACPLAPLFALLNNW 581
              : |     |   || || | |    ||:|||||:||||| |||||| ||||| |||||
Db        648 EHGPERKISFPQWEKDYNLQPMNAYGLYDEYLEMILQFGFTTIFVAAFPLAPLLALLNNI 707

Qy        582 VEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPRAYYR 641
              :|||||| ||| ::|||:| ||:|||| : || |:  |:||:|||::| :|||:||  |
Db        708 IEIRLDAYKFVTQWRRPLASRAKDIGIGYGILEGIGILSVITNAFVIAITSDFIPRLVYA 767
```

```
Qy        642 W----------TRAHDLRGFLNFTLA--------------RAPSSFAAAHNRTCRYRAFR 677
              :                : |::| :|:                  | |:    : |||| :|
Db        768 YKYGPCAGQGEAGQKCMVGYVNASLSVFRISDFENRSEPESDGSEFSGTPLKYCRYRDYR 827

Qy        678 DDDGH-----YSQTYWNLLAIRLAFVIVFEHVVFSVGRLLDLLVPDIPESVEIKVKREYY 732
              |         |:  :|:::|| ||||:|||||:|| :  |:  |:||:|: :  :::|| |
Db        828 DPPHSLVPYGYTLQFWHVLAARLAFIIVFEHLVFCIKHLISYLIPDLPKDLRDRMRREKY 887

Qy        733 LAKQALAENEVLFGTNGTKDEQPKGSELSSHW 764
              | :: : | |:       |: :  |    : |
Db        888 LIQEMMYEAELERLQKERKERKKNGKAHHNEW 919
```

RESULT 8
ADK52114
ID ADK52114 standard; protein; 981 AA.
XX
AC ADK52114;
XX
DT 15-JUN-2007 (revised)
DT 20-MAY-2004 (first entry)
XX
DE Human atopic dermatitis/psoriasis-associated protein #29.
XX
KW Human; atopic dermatitis; psoriasis; dermatological; anti-inflammatory;
KW antipsoriatic; rash; BOND_PC; transmembrane protein 16C;
KW chromosome 11 open reading frame 25;
KW transmembrane protein 16C [Homo sapiens]; TMEM16C; C11orf25; GENX-3947;
KW transmembrane protein 16C (eight membrane-spanning domains);
KW hypothetical protein; hypothetical protein [Homo sapiens]; GO16020;
KW GO16021; GO4185; GO7001.
XX
OS Homo sapiens.
XX
PN WO2004016785-A1.
XX
PD 26-FEB-2004.
XX
PF 06-AUG-2003; 2003WO-JP009999.
XX
PR 06-AUG-2002; 2002JP-00229319.
PR 14-MAY-2003; 2003JP-00136544.
XX
PA (GENO-) GENOX RES INC.
PA (UYJU-) UNIV JUNTENDO.
XX
PI Itoh M, Ogawa K, Shinagawa A, Sudo H, Ogawa H, Ra C;
PI Mitsuishi K;

```
XX
DR   WPI; 2004-214514/20.
DR   N-PSDB; ADK52028.
DR   PC:NCBI; gi13899227.
DR   PC:SWISSPROT; Q9BYT9.
XX
PT   Detecting atopic dermatitis or psoriasis comprises assaying levels of
PT   expression of an indicator gene at a rash site and non-rash site of a
PT   person with atopic dermatitis or psoriasis.
XX
PS   Example 2; SEQ ID NO 147; 484pp; Japanese.
XX
CC   The invention relates to detecting atopic dermatitis or psoriasis
CC   comprising assaying the levels of expression of an indicator gene at a
CC   rash site and non-rash site of a person with atopic dermatitis or
CC   psoriasis, comparing these levels with those of a healthy person, and
CC   determining that if the levels of indicators are higher or lower, then
CC   this indicates the disease. Also included are a reagent for detecting
CC   atopic dermatitis or psoriasis, a kit for screening for treatments, a
CC   transgenic non human vertebrate animal models for the diseases, an agent
CC   for inducing the diseases in mice and a DNA chip for assaying for the
CC   indicator genes. The method is used for treatment, detection and animal
CC   models for research of atopic dermatitis and psoriasis. The present
CC   sequence is a protein encoded by an indicator gene of the invention.
CC
CC   Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC   information from BOND.
XX
SQ   Sequence 981 AA;

  Query Match             35.6%;  Score 1467.5;  DB 8;  Length 981;
  Best Local Similarity   40.9%;  Pred. No. 1.6e-147;
  Matches  313;  Conservative  149;  Mismatches  245;  Indels   59;  Gaps   21;

Qy         20 WAVLCYYAEDLRLKLPLQ----------ELPNQASNWSAGLLAWLGIPNVLLE--VVPDV 67
              |  || ||| | :::| :          :   :   :   :  |:    ::|:    ||:
Db        214 WDTLCKYAERLNIRMPFRKKCYYTDGRSKSMGRMQTYFRRIKDWMAQNPMVLDKSAFPDL 273

Qy         68 -PPEYYSCRFRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTPY--GHEKKNLLGIHQ 124
                 : |:  |   ::  |:  :|:||||::  | :|:: :| :| |  |  |   :|| :
Db        274 EESDCYTGPFSRARIHHFI-INNKDTFFSNATRSRIVYHMLERTKYENGISK---VGIRK 329

Qy        125 LLAEGVLSAAFPLHDGPFKT----PPEGPQAPRLNQRQVLFQHWARWGKWNKYQPLDHVR 180
              |:  |   |||| |:| :|:       |||    | | :|:: ||||| | |:|||| :|
Db        330 LINNGSYIAAFPPHEGAYKSSQPIKTHGPQ----NNRHLLYERWARWGMWYKHQPLDLIR 385

Qy        181 RYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPL 240
               |||||: ||||||||:||| |:|||:||  ||  | | : :   :||:| : : | ||||
Db        386 LYFGEKIGLYFAWLGWYTGMLIPAAIVGLCVFFYGLFTMNNSQVSQEICKATEVF-MCPL 444
```

```
Qy        241 C-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCS 299
              |  :|    |: :|  |:   |||:||||||::|||:|| : ||:|||: : | | ||
Db        445 CDKNCSLQRLNDSCIYAKVTYLFDNGGTVFFAIFMAIWATVFLEFWKRRRSILTYTWDLI 504

Qy        300 DYEDTEERPRPQFAAS-APMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMC 358
              ::|: ||  |||| |    |   |||||: ||: |   :  |:|     |  |:::|:
Db        505 EWEEEEETLRPQFEAKYYKMEIVNPITGKPEPHQPSSDKVTRLLVSVSGIFFMISLVITA 564

Qy        359 LVSIILYR-AIMAIVVSRSGNTLLAAWASRIASLTGSV-VNLVFILILSKIYVSLAHVLT 416
              :  :::||  :|    |   | :   |  : |:   :| :| : |::|:  |  :|::||
Db        565 VFGVVVYRLVVMEQFASFKWNFIKQYW--QFATSAAAVCINFIIIMLLNLAYEKIAYLLT 622

Qy        417 RWEMHRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPGNYHTLFG-VRNEEC 475
              |  ||::::|::| ||:|:|||||  ||  ||||| |||||:|| |: ||   | |||
Db        623 NLEYPRTESEWENSFALKMFLFQFVNLNSSIFYIAFFLGRFVGHPGKYNKLFDRWRLEEC 682

Qy        476 AAGGCLIELAQELLVIMVGKQVINNMQEVLIPKLKGWWQKFRLRSKKRKAGASAGASQGP 535
                ||||:|  :: |||  ||: ||  |:  | :: || : ::     | |    ||
Db        683 HPSGCLIDLCLQMGVIMFLKQIWNNFMELGYPLIQNWWSRHKI-----KRGIH-DASIPQ 736

Qy        536 WEDDYELVP--CEGLFDEYLEMVLQFGFVTIFVAACPLAPLFALLNNWVEIRLDARKFVC 593
              ||:|: | |    || |||||||||||| |||||| ||||| ||||| :|||||| |||
Db        737 WENDWNLQPMNLHGLMDEYLEMVLQFGFTTIFVAAFPLAPLLALLNNIIEIRLDAYKFVT 796

Qy        594 EYRRPVAERAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPRAYYRW----------T 643
              ::|||:  || |||||  || |:  ||||:|||::| :|||::||  | :
Db        797 QWRRPLPARATDIGIWLGILEGIGILAVITNAFVIAITSDYIPRFVYEYKYGPCANHVEP 856

Qy        644 RAHDLRGFLNFTLARAP-SSFAAAHNRTCRYRAFR-----DDDGHYSQTYWNLLAIRLAF 697
              : |:|::| :|:    |      :  |||| :|          ::  ||::|| ||||
Db        857 SENCLKGYVNNSLSFFDLSELGMGKSGYCRYRDYRGPPWSSKPYEFTLQYWHILAARLAF 916

Qy        698 VIVFEHVVFSVGRLLDLLVPDIPESVEIKVKREYYLAKQALAENEV 743
              :|||||:|| :   :  |:||:|: :  :::|| || :: : | |:
Db        917 IIVFEHLVFGIKSFIAYLIPDVPKGLHDRIRREKYLVQEMMYEAEL 962


RESULT 9
AEN06206
ID   AEN06206 standard; protein; 981 AA.
XX
AC   AEN06206;
XX
DT   15-JUN-2007  (revised)
DT   22-FEB-2007  (first entry)
XX
DE   Human esophageal cancer-associated protein SEQ ID NO 231.
XX
```

KW diagnostic; metastasis; esophagus tumor; gastrointestinal disease;
KW neoplasm; cytostatic; cancer; AXL; ZBTB11; TNFRSF14; NSUN5; SPEN; LTBP3;
KW SYNGR1; SLC13A1; MAP3K12; GLYAT; ZNF659; B4GALT2; POGK; AQP3; CAPG;
KW SLIT2; BOND_PC; transmembrane protein 16C;
KW chromosome 11 open reading frame 25;
KW transmembrane protein 16C [Homo sapiens]; TMEM16C; C11orf25; GENX-3947;
KW transmembrane protein 16C (eight membrane-spanning domains);
KW hypothetical protein; hypothetical protein [Homo sapiens]; GO16020;
KW GO16021; GO4185; GO7001.
XX
OS Homo sapiens.
XX
PN WO2006118308-A1.
XX
PD 09-NOV-2006.
XX
PF 02-MAY-2006; 2006WO-JP309177.
XX
PR 02-MAY-2005; 2005JP-00134530.
PR 13-SEP-2005; 2005JP-00265645.
PR 13-SEP-2005; 2005JP-00265678.
XX
PA (TORA) TORAY IND INC.
PA (KYOU) UNIV KYOTO.
XX
PI Akiyama H, Kozono S, Myomoto A, Nomura O, Nobumasa H, Tanaka Y;
PI Tomoda S, Shimada Y, Tsujimoto G;
XX
DR WPI; 2007-110304/11.
DR PC:NCBI; gi13899227.
DR PC:SWISSPROT; Q9BYT9.
XX
PT Composition for determining occurrence/metastasis of esophageal cancer in
PT subject, comprises an antibody binding to a polypeptide encoded by a
PT polynucleotide having a sequence of genes e.g. AXL, ZBTB11 and TNFRSF14,
PT and/or polynucleotides.
XX
PS Claim 1; SEQ ID NO 231; 142pp; Japanese.
XX
CC This invention describes a novel composition for detecting metastasis of
CC esophageal cancer in a test subject. The composition contains a probe
CC derived from polynucleotides AXL, ZBTB11, TNFRSF14, NSUN5, SPEN, LTBP3,
CC SYNGR1, SLC13A1, MAP3K12, GLYAT, ZNF659, B4GALT2, POGK, AQP3, CAPG,
CC SLIT2, their variants or fragments and an antibody. The invention also
CC claims: a) a kit for detecting, determining or presuming the occurrence
CC or metastasis of esophageal cancer in a test subject; b) a DNA chip for
CC detecting, determining or presuming the occurrence or metastasis of
CC esophageal cancer and c) a method to detect, determine or presume the
CC occurrence or metastasis of esophageal cancer in a test subject by

CC detecting the presence of or amount or expression level of one or more
CC esophagus-cancer related target nucleic acid in a biological sample. The
CC method enables the rapid and convenient detection of occurrence or
CC metastasis of esophageal cancer in test subject with high sensitivity.
CC This sequence represents a protein used in the method of the invention
CC
CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 981 AA;

Query Match 35.6%; Score 1467.5; DB 12; Length 981;
Best Local Similarity 40.9%; Pred. No. 1.6e-147;
Matches 313; Conservative 149; Mismatches 245; Indels 59; Gaps 21;

```
Qy         20 WAVLCYYAEDLRLKLPLQ----------ELPNQASNWSAGLLAWLGIPNVLLE--VVPDV 67
              |  || ||| | :::| :           :   :   :   :  |:    ::|:    ||:
Db        214 WDTLCKYAERLNIRMPFRKKCYYTDGRSKSMGRMQTYFRRIKDWMAQNPMVLDKSAFPDL 273

Qy         68 -PPEYYSCRFRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTPY--GHEKKNLLGIHQ 124
                 : |:  |   ::  |:  :|:|||||::  | :|:: :| :| |  |  |   :|| :
Db        274 EESDCYTGPFSRARIHHFI-INNKDTFFSNATRSRIVYHMLERTKYENGISK---VGIRK 329

Qy        125 LLAEGVLSAAFPLHDGPFKT----PPEGPQAPRLNQRQVLFQHWARWGKWNKYQPLDHVR 180
              |:  |   |||| |:| :|:       |||    | | :|:: ||||| | |:|||| :|
Db        330 LINNGSYIAAFPPHEGAYKSSQPIKTHGPQ----NNRHLLYERWARWGMWYKHQPLDLIR 385

Qy        181 RYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPL 240
               |||||: |||||||:||| |:|||:||   ||   | | : :   :||:| : : | ||||
Db        386 LYFGEKIGLYFAWLGWYTGMLIPAAIVGLCVFFYGLFTMNNSQVSQEICKATEVF-MCPL 444

Qy        241 C-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCS 299
              |  :|    |: :|  |:   |||:|||||::|||:|| : ||:|||: : | | ||
Db        445 CDKNCSLQRLNDSCIYAKVTYLFDNGGTVFFAIFMAIWATVFLEFWKRRRSILTYTWDLI 504

Qy        300 DYEDTEERPRPQFAAS-APMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMC 358
              ::|: ||  |||| |    |   |||||: ||: |   :  |:|     |  |:::|:
Db        505 EWEEEEETLRPQFEAKYYKMEIVNPITGKPEPHQPSSDKVTRLLVSVSGIFFMISLVITA 564

Qy        359 LVSIILYR-AIMAIVVSRSGNTLLAAWASRIASLTGSV-VNLVFILILSKIYVSLAHVLT 416
              :  :::||  :|    |   | :   |  : |:   :| :| : |::|:  |  :|::||
Db        565 VFGVVVYRLVVMEQFASFKWNFIKQYW--QFATSAAAVCINFIIIMLLNLAYEKIAYLLT 622

Qy        417 RWEMHRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPGNYHTLFG-VRNEEC 475
                |  ||::::|::| ||:|:|||||  ||  ||||| |||||:|| |: ||   | |||
Db        623 NLEYPRTESEWENSFALKMFLFQFVNLNSSIFYIAFFLGRFVGHPGKYNKLFDRWRLEEC 682

Qy        476 AAGGCLIELAQELLVIMVGKQVINNMQEVLIPKLKGWWQKFRLRSKKRKAGASAGASQGP 535
                 ||||:|  :: |||  ||: ||  |:  | :: || : ::     | |    ||
```

```
Db        683 HPSGCLIDLCLQMGVIMFLKQIWNNFMELGYPLIQNWWSRHKI-----KRGIH-DASIPQ 736

Qy        536 WEDDYELVP--CEGLFDEYLEMVLQFGFVTIFVAACPLAPLFALLNNWVEIRLDARKFVC 593
              ||:|: | |    || |||||||||||| |||||| ||||| ||||| :|||||| |||
Db        737 WENDWNLQPMNLHGLMDEYLEMVLQFGFTTIFVAAFPLAPLLALLNNIIEIRLDAYKFVT 796

Qy        594 EYRRPVAERAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPRAYYRW----------T 643
              ::|||:  || |||||  || |:  ||||:|||::| :||::||  | :
Db        797 QWRRPLPARATDIGIWLGILEGIGILAVITNAFVIAITSDYIPRFVYEYKYGPCANHVEP 856

Qy        644 RAHDLRGFLNFTLARAP-SSFAAAHNRTCRYRAFR-----DDDGHYSQTYWNLLAIRLAF 697
                : |:|::| :|:    |      :  |||| :|          ::  ||:|| ||||
Db        857 SENCLKGYVNNSLSFFDLSELGMGKSGYCRYRDYRGPPWSSKPYEFTLQYWHILAARLAF 916

Qy        698 VIVFEHVVFSVGRLLDLLVPDIPESVEIKVKREYYLAKQALAENEV 743
              :|||||:|| :   :  |:||:|: :  :::|| || :: : | |:
Db        917 IIVFEHLVFGIKSFIAYLIPDVPKGLHDRIRREKYLVQEMMYEAEL 962
```

RESULT 10
AEG11146
ID AEG11146 standard; protein; 840 AA.
XX
AC AEG11146;
XX
DT 15-JUN-2007 (revised)
DT 20-APR-2006 (first entry)
XX
DE Human transmembrane protein 16A, SEQ ID NO: 11.
XX
KW Genetic marker; diagnostic; prognosis; gastrointestinal tumor;
KW cytostatic; neoplasm; tumor marker; transmembrane protein 16A; BOND_PC;
KW TMEM16A protein; TMEM16A protein [Homo sapiens].
XX
OS Homo sapiens.
XX
PN US2006040292-A1.
XX
PD 23-FEB-2006.
XX
PF 08-JUL-2005; 2005US-00177894.
XX
PR 08-JUL-2004; 2004US-0586676P.
XX
PA (WEST/) WEST R B.
PA (VRIJ/) VAN DE RIJN M.
XX
PI West RB, Van De Rijn M;
XX

DR WPI; 2006-182760/19.
DR N-PSDB; AEG11141.
DR GENBANK; AAH33036.
DR PC:NCBI; gi34192278.
XX
PT Classifying tumor as gastrointestinal stromal tumor belonging to PDGFRA
PT positive subclass, involves detecting expression or activity of gene
PT encoding DOG1 polypeptide in sample.
XX
PS Disclosure; SEQ ID NO 11; 177pp; English.
XX
CC The present invention relates to three gene markers such as DOG1, KIT and
CC platelet derived-growth factor receptor alpha (PDGFRA) that are useful in
CC classifying tumors. These gene markers are useful in the classification
CC of gastrointestinal stromal tumors (GISTs) and tumors other than GISTs.
CC The invention also relates to methods providing diagnostic, prognostic
CC and predicative information based on the classifying step. The invention
CC is useful for classifying gastrointestinal stromal tumors as belonging to
CC a PDGFRA positive subclass, KIT negative or PDGFRA negative subclass. The
CC present sequence is human transmembrane protein 16A (DOG1; TMEM16A). The
CC DOG1 gene encodes a transmembrane protein of unknown function
CC (transmembrane protein 16A). The transmembrane protein 16A is encoded by
CC DOG1 gene that is mapped to 11q13.2 on chromosome 11.
CC
CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 840 AA;

Query Match 35.4%; Score 1461.5; DB 11; Length 840;
Best Local Similarity 40.1%; Pred. No. 5.6e-147;
Matches 331; Conservative 149; Mismatches 260; Indels 85; Gaps 21;

```
Qy          5 QDGNTTVH---YALLSASWAVLCYYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVLL 61
              :| :| :|   :  : | | |||  || |:||:| ::: :   | : |||    | :||
Db         28 RDEDTKIHGVGFVKIHAPWNVLCREAEFLKLKMPTKKMYH--INETRGLLK--KINSVLQ 83

Qy         62 EVVPDVPPEYYSCR----------FRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTP 111
              ::   : |:    |          |   |   |  || :|:|| |  |  |::||| :|
Db         84 KITDPIQPKVAEHRPQTMKRLSYPFSREKQHLFDLSD-KDSFFDSKTRSTIVYEILKRTT 142

Qy        112 YGHEKKNLLGIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLNQRQVLFQHWARWGKWN 171
                | : :||  ||| || :||:||||| :       :    | |::|:: |||:| :
Db        143 CTKAKYS-MGITSLLANGVYAAAYPLHDGDY-----NGENVEFNDRKLLYEEWARYGVFY 196

Qy        172 KYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGS 231
              ||||:| ||:|||||: ||||||| ||  |:||::|| :||| ||  :  :||: |:|
Db        197 KYQPIDLVRKYFGEKIGLYFAWLGVYTQMLIPASIVGIIVFLYGCATMDENIPSMEMCDQ 256
```

```
Qy        232 KDSFEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSA 290
              : :  |||||    | :| :||||| |:|  |||:  |||||:|||||   :|:||||
Db        257 RHNITMCPLCDKTCSYWKMSSACATARASHLFDNPATVFFSVFMALWAATFMEHWKRKQM 316

Qy        291 TLAYRWDCSDYEDTEERPRPQFAA-----SAPMTAPNPITGEDEPYFPERSRARRMLAGS 345
               | |||| : :|: |: || :: |      |    : |  |  |:     | |    |
Db        317 RLNYRWDLTGFEEEEDHPRAEYEARVLEKSLKKESRNKET--DKVKLTWRDRFPAYLTNL 374

Qy        346 VVIVVMVAVVVMCLVSIILYRAIMAIVVSRSGNTLLAAWASRIASLTGSVVNLVFILILS 405
              | |: |:||    :: :|:||  ||  :: : :  : :       : |  ::||| |::|
Db        375 VSIIFMIAVTFAIVLGVIIYRISMAAALAMNSSPSVRSNIRVTVTATAVIINLVVIILLD 434

Qy        406 KIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPGNYH 465
              ::|  :|  ||: |: :|:  ||:    | |: :||| |:   |:|||||||| ||:|
Db        435 EVYGCIARWLTKIEVPKTEKSFEERLIFKAFLLKFVNSYTPIFYVAFFKGRFVGRPGDYV 494

Qy        466 TLF-GVRNEECAAGGCLIELAQELLVIMVGKQVI-NNMQEVLIPKLKGWWQKFRLRSKKR 523
               :|   | |||| ||||:||  :| :||:|||:| ||: |: |||:|   :  :|: :
Db        495 YIFRSFRMEECAPGGCLMELCIQLSIIMLGKQLIQNNLFEIGIPKMKKLIRYLKLKQQSP 554

Qy        524 KAGASAGASQGPWEDDYELVPCEGLFDEYLEMVLQFGFVTIFVAACPLAPLFALLNNWVE 583
                    :  :| || | |  ||  ||:||::|||||:||: |||||||||| :|
Db        555 PDHEECVKRKQRYEVDYNLEPFAGLTPEYMEMIIQFGFVTLFVASFPLAPLFALLNNIIE 614

Qy        584 IRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPRA--YYR 641
              |||||:||| | ||||| ||:|||||::|| |:  |||| :||:::|:|||:||    |
Db        615 IRLDAKKFVTELRRPVAVRAKDIGIWYNILRGIGKLAVIIDAFVISFTSDFIPRLVYLYM 674

Qy        642 WTRAHDLRGFLNFTLARAPSSF-------AAAHN----------RTCRYRAFRD---DDGH 682
              :::   : ||:| ||    |||         | |          : |||: :|:    :
Db        675 YSKNGTMHGFVNHTL----SSFNVSDFQNGTAPNDPLDLGYEVQICRYKDYREPPWSENK 730

Qy        683 Y--SQTYWNLLAIRLAFVIVFEHVVFSVGRLLDLLVPDIPESVEIKVKREYYLA------ 734
              |  |: :| :|| ||||||||:::|  :   :| ::|||: :  :: :|  |
Db        731 YDISKDFWAVLAARLAFVIVFQNLVMFMSDFVDWVIPDIPKDISQQIHKEKVLMVELFMR 790

Qy        735 ----KQALAENEVLFGTNGTKDEQP------------KGSELSSH 763
                  || |   |         ||| |             ||   ||
Db        791 EEQDKQQLL--ETCMEKERQKDEPPCNHHNTKACPDSLGSPAPSH 833


RESULT 11
AEG11142
ID   AEG11142 standard; protein; 960 AA.
XX
AC   AEG11142;
XX
DT   15-JUN-2007  (revised)
DT   20-APR-2006  (first entry)
```

XX
DE Human transmembrane protein 16A, SEQ ID NO: 7.
XX
KW Genetic marker; diagnostic; prognosis; gastrointestinal tumor;
KW cytostatic; neoplasm; tumor marker; transmembrane protein 16A; BOND_PC;
KW transmembrane protein 16A;
KW transmembrane protein 16A (eight membrane-spanning domains);
KW oral cancer overexpressed 2; membrane protein;
KW tumor amplified and overexpressed sequence 2;
KW transmembrane protein 16A [Homo sapiens]; TMEM16A; TAOS2; ORAOV2;
KW FLJ10261.
XX
OS Homo sapiens.
XX
PN US2006040292-A1.
XX
PD 23-FEB-2006.
XX
PF 08-JUL-2005; 2005US-00177894.
XX
PR 08-JUL-2004; 2004US-0586676P.
XX
PA (WEST/) WEST R B.
PA (VRIJ/) VAN DE RIJN M.
XX
PI West RB, Van De Rijn M;
XX
DR WPI; 2006-182760/19.
DR N-PSDB; AEG11136.
DR REFSEQ; NP_060513.
DR PC:NCBI; gi40354210.
XX
PT Classifying tumor as gastrointestinal stromal tumor belonging to PDGFRA
PT positive subclass, involves detecting expression or activity of gene
PT encoding DOG1 polypeptide in sample.
XX
PS Disclosure; SEQ ID NO 7; 177pp; English.
XX
CC The present invention relates to three gene markers such as DOG1, KIT and
CC platelet derived-growth factor receptor alpha (PDGFRA) that are useful in
CC classifying tumors. These gene markers are useful in the classification
CC of gastrointestinal stromal tumors (GISTs) and tumors other than GISTs.
CC The invention also relates to methods providing diagnostic, prognostic
CC and predicative information based on the classifying step. The invention
CC is useful for classifying gastrointestinal stromal tumors as belonging to
CC a PDGFRA positive subclass, KIT negative or PDGFRA negative subclass. The
CC present sequence is human transmembrane protein 16A (DOG1; TMEM16A). The
CC DOG1 gene encodes a transmembrane protein of unknown function
CC (transmembrane protein 16A). The transmembrane protein 16A is encoded by

```
CC   DOG1 gene that is mapped to 11q13.2 on chromosome 11.
CC
CC   Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC   information from BOND.
XX
SQ   Sequence 960 AA;

  Query Match             35.3%;  Score 1456.5;  DB 11;  Length 960;
  Best Local Similarity   40.2%;  Pred. No. 2.4e-146;
  Matches  333;  Conservative  147;  Mismatches  260;  Indels   89;  Gaps   22;

Qy          5 QDGNTTVH---YALLSASWAVLCYYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVLL 61
              :| :| :|   :  : | | |||  || |:||:| ::: :   | : |||    | :||
Db        144 RDEDTKIHGVGFVKIHAPWNVLCREAEFLKLKMPTKKMYH--INETRGLLK--KINSVLQ 199

Qy         62 EVVPDVPPEYYSCR----------FRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTP 111
              ::   : |:    |          |   |   |  || :|:|| |  |  |::||| :|
Db        200 KITDPIQPKVAEHRPQTMKRLSYPFSREKQHLFDLSD-KDSFFDSKTRSTIVYEILKRTT 258

Qy        112 YGHEKKNLLGIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLNQRQVLFQHWARWGKWN 171
                  | : :||  ||| || :|||:||||| :       :    | |::|:: |||:| :
Db        259 CTKAKYS-MGITSLLANGVYAAAYPLHDGDY-----NGENVEFNDRKLLYEEWARYGVFY 312

Qy        172 KYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGS 231
              ||||:| ||:|||||: ||||||| ||  |:||::|| :||| ||  :  :||: |:|
Db        313 KYQPIDLVRKYFGEKIGLYFAWLGVYTQMLIPASIVGIIVFLYGCATMDENIPSMEMCDQ 372

Qy        232 KDSFEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSA 290
              : :  |||||    | :| :||||| |:|  |||:  |||||:||||||    :|:||||
Db        373 RHNITMCPLCDKTCSYWKMSSACATARASHLFDNPATVFFSVFMALWAATFMEHWKRKQM 432

Qy        291 TLAYRWDCSDYEDTEE----RPRPQFAA-----SAPMTAPNPITGEDEPYFPERSRARRM 341
               | |||| : :|: ||     || :: |     |    : |  |  |:      | |
Db        433 RLNYRWDLTGFEEEEEAVKDHPRAEYEARVLEKSLKKESRNKET--DKVKLTWRDRFPAY 490

Qy        342 LAGSVVIVVMVAVVVMCLVSIILYRAIMAIVVSRSGNTLLAAWASRIASLTGSVVNLVFI 401
              |   | |: |:||    :: :|:||  ||  :: : :  : :       : |  ::||| |
Db        491 LTNLVSIIFMIAVTFAIVLGVIIYRISMAAALAMNSSPSVRSNIRVTVTATAVIINLVVI 550

Qy        402 LILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYP 461
              ::| ::|  :|  ||: |: :|:  ||:    | |: :||| |:   |:|||||||| |
Db        551 ILLDEVYGCIARWLTKIEVPKTEKSFEERLIFKAFLLKFVNSYTPIFYVAFFKGRFVGRP 610

Qy        462 GNYHTLF-GVRNEECAAGGCLIELAQELLVIMVGKQVI-NNMQEVLIPKLKGWWQKFRLR 519
              |:|  :|   | |||| ||||:||  :| :||:|||:| ||: |: |||:|   :  :|:
Db        611 GDYVYIFRSFRMEECAPGGCLMELCIQLSIIMLGKQLIQNNLFEIGIPKMKKLIRYLKLK 670

Qy        520 SKKRKAGASAGASQGPWEDDYELVPCEGLFDEYLEMVLQFGFVTIFVAACPLAPLFALLN 579
               :           :  :| || | |  ||  ||:||::|||||:|||: ||||||||||
```

```
Db        671 QQSPPDHEECVKRKQRYEVDYNLEPFAGLTPEYMEMIIQFGFVTLFVASFPLAPLFALLN 730

Qy        580 NWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPRA- 638
              | :|||||:||| | ||||| ||:|||||::|| |:  |||| |||:::|:|||:|| 
Db        731 NIIEIRLDAKKFVTELRRPVAVRAKDIGIWYNILRGIGKLAVIINAFVISFTSDFIPRLV 790

Qy        639 -YYRWTRAHDLRGFLNFTLARAPSSF--------AAAHN---------RTCRYRAFRD--- 678
               | :::   : ||:| ||    |||         | |          : |||: :|:
Db        791 YLYMYSKNGTMHGFVNHTL----SSFNVSDFQNGTAPNDPLDLGYEVQICRYKDYREPPW 846

Qy        679 DDGHY--SQTYWNLLAIRLAFVIVFEHVVFSVGRLLDLLVPDIPESVEIKVKREYYLA-- 734
               :  |  |: :| :|| |||||||:::|  :   :| ::|||: :  :: :|  |
Db        847 SENKYDISKDFWAVLAARLAFVIVFQNLVMFMSDFVDWVIPDIPKDISQQIHKEKVLMVE 906

Qy        735 --------KQALAENEVLFGTNGTKDEQP----------KGSELSSH 763
                     || |   |        ||| |            ||   ||
Db        907 LFMREEQDKQQLL--ETWMEKERQKDEPPCNHHNTKACPDSLGSPAPSH 953
```

```
RESULT 12
AFB77190
ID   AFB77190 standard; protein; 1017 AA.
XX
AC   AFB77190;
XX
DT   28-JUN-2007  (first entry)
XX
DE   Mouse TM-1 (Tmem16a) protein.
XX
KW   Cell isolation; stem cell; therapeutic; transgenic animal; screening;
KW   tissue regeneration; genitourinary disease; uropathic;
KW   intervertebral disk displacement; degeneration; injury; vulnerary;
KW   back pain; transmembrane factor-1; Tmem16a.
XX
OS   Mus musculus.
XX
PN   WO2007027583-A2.
XX
PD   08-MAR-2007.
XX
PF   28-AUG-2006; 2006WO-US033491.
XX
PR   31-AUG-2005; 2005US-0713400P.
XX
PA   (UYFL ) UNIV FLORIDA RES FOUND INC.
XX
PI   Harfe BD,  Cohn MJ;
XX
DR   WPI; 2007-412931/39.
```

DR N-PSDB; AFB77189.
XX
PT Isolating sonic hedgehog expressing-cells comprises obtaining a non-human
PT transgenic subject in which a marker gene has been inserted into the
PT subject's genome.
XX
PS Disclosure; SEQ ID NO 2; 96pp; English.
XX
CC The present invention relates to a method of isolating cells in selected
CC tissues co-expressing the sonic hedgehog (Shh) gene and a marker gene.
CC The method involves obtaining a non-human transgenic subject in which a
CC marker gene has been inserted into the subject's genome and isolating
CC Shh/marker gene expressing cells and Shh/marker gene non-expressing cells
CC from the selected tissue. The invention further provides a method of
CC identifying differentially expressed genes (e.g. transmembrane factors TM
CC -1 and TM-2, EST 1437418, Mmu-miR-135a-2 and AP-2 beta) in selected
CC tissues co-expressing the sonic hedgehog gene and a marker gene. The
CC invention is useful in tissue engineering, regeneration, reconstruction
CC and/or repair of tissues and genitourinary system and also in treating
CC intervertebral disk rupture, degeneration, disease or injury and back
CC pain. The invention is further useful for generating transgenic animal.
CC The present sequence is the mouse TM-1 (Tmem16a) protein.
XX
SQ Sequence 1017 AA;

Query Match 35.2%; Score 1452.5; DB 12; Length 1017;
Best Local Similarity 40.0%; Pred. No. 7e-146;
Matches 330; Conservative 156; Mismatches 257; Indels 81; Gaps 22;

```
Qy          6 DGNTTVH---YALLSASWAVLCYYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVLLE 62
              | :| :|   :  : | | |||  || |:||:| ::: : :   : |||    | :|| :
Db        202 DEDTKIHGVGFVKIHAPWHVLCREAEFLKLKMPTKKVYHISE--TRGLLK--TINSVLQK 257

Qy         63 VVPDVPPEYYSCRFRVNKLPRFLGS---------DNQDTFFTSTKRHQILFEILAKTPYG 113
              :   : |:    | :  |   :  |          ::|:|| |  |  |::||| :|
Db        258 ITDPIQPKVAEHRPQTTKRLSYPFSREKQHLFDLTDRDSFFDSKTRSTIVYEILKRTTCT 317

Qy        114 HEKKNLLGIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLNQRQVLFQHWARWGKWNKY 173
              | : :||  ||| || |||:|||| :    ||       | |::|:: || :| : ||
Db        318 KAKYS-MGITSLLANGVYSAAYPLHDGDY----EGDNV-EFNDRKLLYEEWASYGVFYKY 371

Qy        174 QPLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKD 233
              ||:| ||:|||||| ||||||| ||  |:||::|| :||| ||  |  :||: |:|  :
Db        372 QPIDLVRKYFGEKVGLYFAWLGAYTQMLIPASIVGVIVFLYGCATVDENIPSMEMCDQRY 431

Qy        234 SFEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATL 292
              :  |||||   | :| :|||||  |:|  |||:  |||||:||||||   :|:||||   |
Db        432 NITMCPLCDKTCSYWKMSSACATARASHLFDNPATVFFSVFMALWAATFMEHWKRKQMRL 491
```

```
Qy        293 AYRWDCSDYEDTEE----RPRPQFAA-----SAPMTAPNPITGEDEPYFPERSRARRMLA 343
              |||| : :|: ||      || :: |      |    : |  |  |:      | |
Db        492 NYRWDLTGFEEEEEAVKDHPRAEYEARVLEKSLRKESRNKET--DKVKLTWRDRFPAYFT 549

Qy        344 GSVVIVVMVAVVVMCLVSIILYRAIMAIVVSRSGNTLLAAWASRIASLTGSVVNLVFILI 403
                | |: |:||    :: :|:||   |  :: : :  : :       : |  ::||| |::
Db        550 NLVSIIFMIAVTFAIVLGVIIYRISTAAALAMNSSPSVRSNIRVTVTATAVIINLVVIIL 609

Qy        404 LSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPGN 463
              | ::|  :|  ||: |: :|:  ||:  | | |: :||| |:   |:|||||||| ||:
Db        610 LDEVYGCIARWLTKIEVPKTEKSFEERLTFKAFLLKFVNSYTPIFYVAFFKGRFVGRPGD 669

Qy        464 YHTLF-GVRNEECAAGGCLIELAQELLVIMVGKQVI-NNMQEVLIPKLKGWWQKFRLRSK 521
              |  :|   | |||| ||||:||  :| :||:|||:| ||: |: |||:| : :  :|| :
Db        670 YVYIFRSFRMEECAPGGCLMELCIQLSIIMLGKQLIQNNLFEIGIPKMKKFIRYLKLRRQ 729

Qy        522 KRKAGASAGASQGPWEDDYELVPCEGLFDEYLEMVLQFGFVTIFVAACPLAPLFALLNNW 581
                        :  :| |: | |  ||  ||:|::|||||:|||: ||||||||||
Db        730 SPSDREEYVKRKQRYEVDFNLEPFAGLTPEYMEMIIQFGFVTLFVASFPLAPLFALLNNI 789

Qy        582 VEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPRAYYR 641
              :||||||||| | ||||| |||:|||||::|| |:  |||| |||:::|:|||:||  |
Db        790 IEIRLDAKKFVTELRRPVAIRAKDIGIWYNILRGVGKLAVIINAFVISFTSDFIPRLVYL 849

Qy        642 WTRAHD--LRGFLNFTLARAPSSF-------AAAHN---------RTCRYRAFRD---DD 680
              :  : :  : ||:| ||    |||          | |          : |||: :|:    :
Db        850 YMYSQNGTMHGFVNHTL----SSFNVSDFQNGTAPNDPLDLGYEVQICRYKDYREPPWSE 905

Qy        681 GHY--SQTYWNLLAIRLAFVIVFEHVVFSVGRLLDLLVPDIPESVEIKVKREYYL----- 733
                |  |: :| :|| ||||||||:::|  :   :| ::|||||: :  :: :|  |
Db        906 HKYDISKDFWAVLAARLAFVIVFQNLVMFMSDFVDWVIPDIPKDISQQIHKEKVLMVELF 965

Qy        734 -----AKQALAENEVLFGTNGTKDEQPKGSELSSHWTPFTVPKA 772
                    || | :  :        : |:|:    ::| :| | |:|
Db        966 MREEQGKQQLLDTWM-------EKEKPRDVPCNNH-SPTTHPEA 1001


RESULT 13
ADG48280
ID   ADG48280 standard; protein; 1003 AA.
XX
AC   ADG48280;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Human retina-specific protein - C12orf3variants.
XX
KW   human; retina-specific protein; NETO1; retinal disease;
KW   age related macular degeneration; night blindness; C12orf3variants.
```

XX
OS Homo sapiens.
XX
PN WO2003068967-A2.
XX
PD 21-AUG-2003.
XX
PF 18-FEB-2003; 2003WO-EP001625.
XX
PR 18-FEB-2002; 2002EP-00003675.
PR 21-FEB-2002; 2002US-0357857P.
XX
PA (LYNK-) LYNKEUS BIO TECH GMBH.
XX
PI Stoehr BH, Weber FHB, Goehring F;
XX
DR WPI; 2003-767334/72.
DR N-PSDB; ADG48279.
XX
PT New nucleic acid encoding retinal protein sNETO1, useful for diagnosis of
PT retinal disease, especially macular degeneration, also for drug screening
PT and therapy.
XX
PS Claim 18; Fig 14; 199pp; English.
XX
CC The invention comprises the amino acid and coding sequences of a human
CC retina-specific protein - NETO1. The DNA and protein sequences of the
CC invention are useful in the treatment of retinal diseases, such as
CC macular degeneration (especially age related) and night blindness. The
CC present amino acid sequence represents the human retina-specific protein
CC C12orf3variants.
XX
SQ Sequence 1003 AA;

Query Match 34.9%; Score 1437; DB 7; Length 1003;
Best Local Similarity 38.7%; Pred. No. 3.2e-144;
Matches 326; Conservative 161; Mismatches 263; Indels 92; Gaps 23;

```
Qy          1 QQDVQDGNTTVHYALLSASWAVLCYYAEDLRLKLPLQELPNQ-------ASNWSAGLLAW 53
              ::|::: :    :  : | | ||   || |::|:| ::   :       |  :|| |
Db        174 EKDLENKSQGSIFVRIHAPWQVLAREAEFLKIKVPTKKEMYEIKAGGSIAKKFSAAL--- 230

Qy         54 LGIPNVLLEVVPDVPPEYYSCRFRVNKLP------RFLGSDNQDTFFTSTKRHQILFEIL 107
                    :   : | | ||: : : :    |             :|||| :  | :|: |||
Db        231 ---QKLSSHLQPRV-PEHSNNKMKNLSYPFSREKMYLYNIQEKDTFFDNATRSRIVHEIL 286

Qy        108 AKTPYGHEKKNLLGIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLNQRQVLFQHWARW 167
               :|       | :||: |:|  :  ||:|||| : :| :      :| |::|:| |||:
Db        287 KRTACS-RANNTMGINSLIANNIYEAAYPLHDGEYDSPEDD-----MNDRKLLYQEWARY 340
```

```
Qy        168 GKWNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQE 227
              | : |:|||:| :|:|||||: ||||||| || :|:|::|:| :||| ||  :  |||::|
Db        341 GVFYKFQPIDLIRKYFGEKIGLYFAWLGLYTSFLIPSSVIGVIVFLYGCATIEEDIPSRE 400

Qy        228 LCGSKDSFEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWK 286
              :|  :::| |||||   | :| |||||  |||  |||:  |||||:|||||| : || ||
Db        401 MCDQQNAFTMCPLCDKSCDYWNLSSACGTAQASHLFDNPATVFFSIFMALWATMFLENWK 460

Qy        287 RKSATLAYRWDCSDYEDTEER----PRPQFAA------------SAPMTAPNPIT----G 326
              |    | | || :  |: |||      ||::               ||        |
Db        461 RLQMRLGYFWDLTGIEEEEERAQEHSRPEYETKVREKMLKESNQSAVQKLETNTTECGDE 520

Qy        327 EDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLVSIILYRAIMAIVVSRSGNTLLAAWAS 386
              :||     : |    |     |: |:|:    :  :|:||   |  :|     | | |
Db        521 DDEDKLTWKDRFPGYLMNFASILFMIALTFSIVFGVIVYRITAAALS-----LNKATRS 575

Qy        387 RI---ASLTGSVVNLVFILILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNF 443
              :    : |  ::||| |||| :|| ::|  ||: |: :|:  ||:   || |: :|||
Db        576 NVRVTVTATAVIINLVVILILDEIYGAVAKWLTKIEVPKTEQTFEERLILKAFLLKFVNA 635

Qy        444 YSSPVYIAFFKGRFVGYPGNYHTLF-GVRNEECAAGGCLIELAQELLVIMVGKQVI-NNM 501
              ||   |:|||||||| ||:|  :| | | |||| ||||:||  :| :||:|||::| ||:
Db        636 YSPIFYVAFFKGRFVGRPGSYVYVFDGYRMEECAPGGCLMELCIQLSIIMLGKQLIQNNI 695

Qy        502 QEVLIPKLKGWWQKFRLRSKKRKAGASAGA-SQGP--WEDDYELVPCEGLFDEYLEMVLQ 558
               |: :||||   : ||    : :|| :  | |: |  |: || | |  ||  ||:|||::|
Db        696 FEIGVPKLK---KLFRKLKDETEAGETDSAHSKHPEQWDLDYSLEPYTGLTPEYMEMIIQ 752

Qy        559 FGFVTIFVAACPLAPLFALLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTH 618
              |||||:|||: ||||:|||||| :|:||||:||| | ||| | | :|||||| ||:|:
Db        753 FGFVTLFVASFPLAPVFALLNNVIEVRLDAKKFVTELRRPDAVRTKDIGIWFDILSGIGK 812

Qy        619 LAVISNAFLLAFSSDFLPRAYYRWTRAHD--LRGFLNFTLA-----------RAPSSFAA 665
              :|||||::| :|||:||  |::: :|:  | ||:| ||:           :  :|
Db        813 FSVISNAFVIAITSDFIPRLVYQYSYSHNGTLHGFVNHTLSFFNVSQLKEGTQPENSQFD 872

Qy        666 AHNRTCRYRAFRD-----DDGHYSQTYWNLLAIRLAFVIVFEHVVFSVGRLLDLLVPDIP 720
                 : ||:: :|:     :   :|: || :|: |||||:|:::|  :  |:| ::||||
Db        873 QEVQFCRFKDYREPPWAPNPYEFSKQYWFILSARLAFVIIFQNLVMFLSVLVDWMIPDIP 932

Qy        721 ESVEIKVKRE------YYLAKQALAENEVLFGTNGTKDEQPKGSELSSHWTPFTVPKA-S 773
              :  ::|:|      ::| :    |:| |   :      | | : |      : |   |
Db        933 TDISDQIKKEKSLLVDFFLKE----EHEKLKLMDEPALRSPGGGDRSRSRAASSAPSGQS 988

Qy        774 QL 775
              ||
Db        989 QL 990
```

```
RESULT 14
AEH82071
ID   AEH82071 standard; protein; 913 AA.
XX
AC   AEH82071;
XX
DT   15-JUN-2007  (revised)
DT   13-JUL-2006  (first entry)
XX
DE   Human gnathodiaphyseal dysplasia protein, GDD1.
XX
KW   Osteopathic; Gene therapy; bone disease; bone injury; bone resorption;
KW   gnathodiaphyseal dysplasia; GDD1; BOND_PC; transmembrane protein 16E;
KW   integral membrane protein GDD1; transmembrane protein 16E [Homo sapiens];
KW   TMEM16E; GDD1; integral membrane protein GDD1 [Homo sapiens]; GO5783;
KW   GO16020; GO16021.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Inhibitory-site 356
FT                   /note= "Missense mutations in the coding sequence can
FT                   lead to substitution of this residue with either Arg or
FT                   Gly"
XX
PN   JP2006121961-A.
XX
PD   18-MAY-2006.
XX
PF   28-OCT-2004; 2004JP-00313511.
XX
PR   28-OCT-2004; 2004JP-00313511.
XX
PA   (UYTO-) UNIV TOKUSHIMA NAT UNIV CORP.
XX
PI   Itakura M,  Tsutsumi S,  Kamata N,  Inoue H;
XX
DR   WPI; 2006-367194/38.
DR   N-PSDB; AEH82070.
DR   PC:NCBI; gi47106048.
DR   PC:SWISSPROT; Q75V66.
XX
PT   Novel gnathodiaphseal dysplasia DNA, useful as diagnostic agent for bone
PT   disease such as gnathodiaphseal dysplasia, bone deficiency or bone-
PT   resorption property disease.
XX
PS   Claim 9; SEQ ID NO 2; 11pp; Japanese.
XX
```

```
CC   The present invention relates to a human gnathodiaphyseal dysplasia (GDD)
CC   coding sequence (GDD1; AEH82070) and encoded protein (AEH82071). GDD1 is
CC   useful as a bone disease diagnostic agent, where the bone disease is GDD,
CC   bone deficiency and/or bone-resorption property disease, where the GDD
CC   disease causes hardening of bone, susceptibility to fracture, cement bone
CC   pathology of a lower jaw bone, etc. GDD1 is also useful in bone formation
CC   regeneration, hard tissue reconstruction, etc., and in research
CC   application.
CC
CC   Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC   information from BOND.
XX
SQ   Sequence 913 AA;

  Query Match             34.3%;  Score 1412.5;  DB 11;  Length 913;
  Best Local Similarity   39.2%;  Pred. No. 1.2e-141;
  Matches  309;  Conservative  148;  Mismatches  259;  Indels   73;  Gaps   20;

Qy          1 QQDVQDGNTTVHYALLSASWAVLCYYAEDLRLKLPLQE--LPNQASNWSAGLLAWLGIPN 58
              ::| :|| |  ::  : | | ||  ||| | :|:|::|  :|       : :|  : :|
Db        120 KRDSEDGRT--YFVKIHAPWEVLVTYAEVLGIKMPIKESDIPRPKHTPISYVLGPVRLP- 176

Qy         59 VLLEVVPDVPPEYYSCRFRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTPYGHEK-K 117
               |    |   |||:: :|  ::   ||  | | ||| |: |::|:: ||:: |:| |  |
Db        177 -LSVKYPH--PEYFTAQFSRHRQELFLIED-QATFFPSSSRNRIVYYILSRCPFGIEDGK 232

Qy        118 NLLGIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLNQRQVLFQHWARWGKWNKYQPLD 177
                 || :||     |:|:|||| :  | | |     |:|  | |:|||:  : | ||||
Db        233 KRFGIERLLNSNTYSSAYPLHDGQYWKPSEPPNP--TNERYTLHQNWARFSYFYKEQPLD 290

Qy        178 HVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSK--DSF 235
              :: |:|||: :|| :|||||  |  |||||   |: |   :  :  : |:|  :
Db        291 LIKNYYGEKIGIYFVFLGFYTEMLFFAAVVGLACFIYGLLSMEHNTSSTEICDPEIGGQM 350

Qy        236 EMCPLCLD-CPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAY 294
               |||||    | :| |:| |  ::   |||:  ||||::|| :|  | ||:|||:: | | |
Db        351 IMCPLCDQVCDYWRLNSTCLASKFSHLFDNESTVFFAIFMGIWVTLFLEFWKQRQARLEY 410

Qy        295 RWDCSDYEDTEE--RPRPQFAASAPMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMV 352
              ||  |:|: ::  : ||:| |       | :| | ||| |  :|          : : :
Db        411 EWDLVDFEEEQQQLQLRPEFEAMCKHRKLNAVTKEMEPYMPLYTRIPWYFLSGATVTLWM 470

Qy        353 AVVVMCLVSIILYRAIMAIVVSRSGNTLLAAWASRI------------------ASLTGS 394
              ::||  :|::|:||             :: | :|| :                  |||||
Db        471 SLVVTSMVAVIVYRL-----------SVFATFASFMESDASLKQVKSFLTPQITTSLTGS 519

Qy        395 VVNLVFILILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFK 454
              :| : ||||:  |  ::  :|: |: ||  ::| : |||:|:|||||||||  |:||||
Db        520 CLNFIVILILNFFYEKISAWITKMEIPRTYQEYESSLTLKMFLFQFVNFYSSCFYVAFFK 579
```

```
Qy        455 GRFVGYPGNYHTLFGV-RNEECAAGGCLIELAQELLVIMVGKQVINNMQEVLIPKLKGWW 513
              |:|||||| |   ||    |:|||  |||||||  :| :|| |||:  |::| : |    ||
Db        580 GKFVGYPGKYTYLFNEWRSEECDPGGCLIELTTQLTIIMTGKQIFGNIKEAIYPLALNWW 639

Qy        514 QKFRLRSKKRKAGASAGASQGPWEDDYELVPCE--GLFDEYLEMVLQFGFVTIFVAACPL 571
                     ::|||  ::       || |::|      ||| |||| | ||||||:|||: ||
Db        640 -------RRRKARTNSEKLYSRWEQDHDLESFGPLGLFYEYLETVTQFGFVTLFVASFPL 692

Qy        572 APLFALLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISNAFLLAFS 631
              ||| ||:|| ||||:|| |   :||| || :|  ||:|  || |:  |:| :|||::||:
Db        693 APLLALINNIVEIRVDAWKLTTQYRRTVASKAHSIGVWQDILYGMAVLSVATNAFIVAFT 752

Qy        632 SDFLPRAYYRW----TRAHDLRGFLN-----FTLARAPSSFAAAHNR---TCRYRAFR-- 677
              || :||  | :          : |::|     | :|  |:  | :  |   |||| :|
Db        753 SDIIPRLVYYYAYSTNATQPMTGYVNNSLSVFLIADFPNHTAPSEKRDFITCRYRDYRYP 812

Qy        678 -DDDGHY--SQTYWNLLAIRLAFVIVFEHVVFSVGRLLDLLVPDIPESVEIKVKREYYLA 734
               ||:  |  :  :|::|| :: |:|| ||||| |  ||  ::||:|: |  ::|||  :
Db        813 PDDENKYFHNMQFWHVLAAKMTFIIVMEHVVFLVKFLLAWMIPDVPKDVVERIKREKLMT 872

Qy        735 KQALAENEV 743
               : | : |:
Db        873 IKILHDFEL 881
```

RESULT 15
ABB62812
ID   ABB62812 standard; protein; 1219 AA.
XX
AC   ABB62812;
XX
DT   15-JUN-2007 (revised)
DT   26-MAR-2002 (first entry)
XX
DE   Drosophila melanogaster polypeptide SEQ ID NO 15228.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical; BOND_PC; CG6938-PA; CG6938-PA [Drosophila melanogaster];
KW   CG6938.
XX
OS   Drosophila melanogaster.
XX
PN   WO200171042-A2.
XX
PD   27-SEP-2001.
XX
PF   23-MAR-2001; 2001WO-US009231.
XX

```
PR   23-MAR-2000; 2000US-0191637P.
PR   11-JUL-2000; 2000US-00614150.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Venter JC,  Adams M,  Li PWD,  Myers EW;
XX
DR   WPI; 2001-656860/75.
DR   N-PSDB; ABL06915.
DR   PC:NCBI; gi24663059.
XX
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signaling and cell-cell
PT   interactions.
XX
PS   Disclosure; SEQ ID NO 15228; 21pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC   ABB72072). The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences
CC
CC   Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC   information from BOND.
XX
SQ   Sequence 1219 AA;

  Query Match             33.4%;  Score 1378.5;  DB 4;  Length 1219;
  Best Local Similarity   37.8%;  Pred. No. 8.5e-138;
  Matches  304;  Conservative  146;  Mismatches  284;  Indels   71;  Gaps   19;

Qy          5 QDGNTTVHYALLSASWAVLCYYAEDLRLKLP-------------------LQELPNQASN 45
              |  |    :  :   | :    || : ||||                    |: :
Db        384 QSFNEKTFFLKIHLPWRLETRLAEVMNLKLPVKRFITISVKPSWDEENVVLRNMQYWKDV 443

Qy         46 WSAGLLAWLGIPNVLLEVVPDVPPEYYSCRFRVNKLPRFLGSDNQDTFFTSTKRHQILFE 105
              |   |   : :   |||         : :      |   :|:  | : | ||| :|  :: :
Db        444 WQR-LTKKIQLDQTLLE----GETTFKAATANGNPEEQFIVKD-RATAFTSAQRSLMVMQ 497

Qy        106 ILAKTPYGHEKKNLLGIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLN-QRQVLFQHW 164
              :| :||:    ::  || :|: :|     |||:| :    : | :  ::  |:||:| |
Db        498 VLIRTPFDESDRS--GIRRLMNDGTYLGCFPLHEGRY----DRPHSSGISLDRRVLYQTW 551
```

```
Qy        165 ARWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSD-- 222
              |   :| | |||   ||:|||:|:|||| ||||||  |:  |||||| |: |    : |:
Db        552 AHPSQWYKKQPLCLVRKYFGDKIALYFCWLGFYTEMLVYPAVVGTLCFIYGLATLESEDN 611

Qy        223 IPTQELCG--SKDSFEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAV 279
               |::|:|       :  :|||   | :  || :|  ::   |||:  ||||::||: ||
Db        612 TPSKEICNEYGTGNITLCPLCDKACSYQRLSESCLFSRLTYLFDNPSTVFFAIFMSFWAT 671

Qy        280 LLLEYWKRKSATLAYRWDCSDYEDTEERPRPQFAASAPMTAPNPITGEDEPYFPERSRAR 339
              || |||| : | : ||   :  | :|  ||:|  :|     ||:| | |||    :|:
Db        672 TFLELWKRKQSVLVWEWDLHNV-DMDEENRPEFETNATTFRMNPVTREKEPYMSTWNRSI 730

Qy        340 RMLAGSVVIVVMVAVVVMCLVSIILYRAIMAIVVSRSGNTLLAAWASRIASLTGSVVNLV 399
              | :     :: |::||:  ::  ||||  :  |:   |   :   |    |:| :::|||
Db        731 RFVITGSAVLFMISVVLSAVLGTILYRITLVSVIYGGGGFFVKEHAKLFTSVTAALINLV 790

Qy        400 FILILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVG 459
               |:||::||  :|  ||  |  || |::||::| |:| |:|:|||| :|||||||||
Db        791 VIMILTRIYHRMAIKLTNLENPRTHTEYEDSYTFKIFFFEFMNFYSSLIYIAFFKGRFFD 850

Qy        460 YPGNYHT----LFGVRNEECAAGGCLIELAQELLVIMVGKQVINNMQEVLIPKLKGWWQK 515
              |||:         | ::|: |   ||| ||  :| :||||||  ||  | | ||   ||:
Db        851 YPGDDQARKSEFFRLKNDICDPAGCLSELCIQLAIIMVGKQCWNNFMEYLFPKFWNWWR- 909

Qy        516 FRLRSKKRKAGASAGASQGPWEDDYELV-PCE-GLFDEYLEMVLQFGFVTIFVAACPLAP 573
               : | ::|          || || :  |    ||||||||:||:||||:|||| ||||
Db        910 ---QRKHKQATKDESHLHMAWEQDYHMQDPGRLALFDEYLEMILQYGFVTLFVAAFPLAP 966

Qy        574 LFALLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISNAFLLAFSSD 633
              |||||||  |||||| | | : |||:||| :||| |: ||  :|: ||:||||::|::||
Db        967 LFALLNNVAEIRLDAYKMVTQARRPLAERVEDIGAWYGILRIITYTAVVSNAFVIAYTSD 1026

Qy        634 FLPRAYYR--WTRAHDLRGFLNFTLA---------RAPSSFAAAHNRTCRYRAFRDDDGH 682
              |:||  |:  ::  | | |::  :|:            :| :     ||:|| :|:
Db       1027 FIPRMVYKFVYSETHTLAGYIEHSLSIFNTSDYKEEWGASVSEKDPDTCQYRGYRNGPKD 1086

Qy        683 Y-----SQTYWNLLAIRLAFVIVFEHVVFSVGRLLDLLVPDIPESVEIKVKREYYLAKQA 737
              |     |  ||:: | |||||:|||||| :  ::  ::|||:|  |: :::||  |||:|
Db       1087 YEPYGLSPHYWHVFAARLAFVVVFEHVVFVITGIMQFIIPDVPSEVKTQMQREQLLAKEA 1146

Qy        738 LAENEVLFGTNGTKDEQPKGSELSS 762
               :       :| |  |    :: |
Db       1147 KYQ-------HGIKRAQGDSQDIMS 1164


Search completed: June 24, 2008, 15:22:07
Job time : 273 secs
```

SCORE 3.0